

SEQUENCE LISTING

<110> Micromet AG

<120> Multispecific deimmunized CD3 binders

<130> G 2728 PCT

<160> 409

<170> PatentIn version 3.1

<210> 1

<211> 729

<212> DNA

<213> artificial sequence

<220>

<223> wt Anti-CD3 cassette

<400> 1

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cctggacagg gtctggaatg gattggatac attaatccta gccgtgggta tactaattac	180
aatcagaagt tcaaggacaa ggccacattg actacagaca aatcctccag cacagcctac	240
atgcaactga gcagcctgac atctgaggac tctgcagtct attactgtgc aagatattat	300
gatgatcatt actgccttga ctactggggc caaggcacca ctctcacagt ctccctcagtc	360
gaaggtggaa gtggaggttc tgggtggaagt ggaggttcag gtggagtcga cgacattcag	420
ctgacccagt ctccagcaat catgtctgca tctccagggg agaaggtcac catgacctgc	480
agagccagtt caagtgtaag ttacatgaac tgggtaccagc agaagtcagg cacctcccc	540
aaaagatgga tttatgacac atccaaagtg gcttctggag tcccttatcg cttcagtggc	600
agtgggtctg ggacctcata ctctctcaca atcagcagca tggaggctga agatgctgcc	660
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gagctgaaa	729

<210> 2

<211> 243

<212> PRT

<213> artificial sequence

<220>

<223> wt Anti-CD3 cassette

<400> 2

Asp Ile Lys Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala

1	5	10	15
Ser Val Lys Met Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Arg Tyr	20	25	30
Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile	35	40	45
Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe	50	55	60
Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr	65	70	75
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys	85	90	95
Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly	100	105	110
Thr Thr Leu Thr Val Ser Ser Val Glu Gly Gly Ser Gly Gly Ser Gly	115	120	125
Gly Ser Gly Gly Ser Gly Gly Val Asp Asp Ile Gln Leu Thr Gln Ser	130	135	140
Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys	145	150	155
Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser	165	170	175
Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser	180	185	190
Gly Val Pro Tyr Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser	195	200	205
Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys	210	215	220
Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu	225	230	235
			240

Glu Leu Lys

<210> 3
 <211> 18
 <212> PRT
 <213> artificial sequence

<220>
 <223> deimmunized linker

<400> 3

Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly
 1 5 10 15

Ala Asp

<210> 4
 <211> 729
 <212> DNA
 <213> artificial sequence

<220>
 <223> VH2/VL1

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 cctggacagg gtctggaatg gattggatac attaataccta gccgtgggtta tactaattac 180
 gcacagaagt tgcagggccg cgtcacaatg actacagaca cttccaaccag cacagcctac 240
 atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300
 gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctcctcaggc 360
 gaaggtacta gtactgggtc tgggtggaagt ggaggttcag gtggagcaga cgacattcag 420
 atgaccagtc ctccatctag cctgtctgca tctgtcgggg accgtgtcac catcacctgc 480
 agagccagtc aaagtgtaag ttacatgaac tgggtaccagc agaagccggg caaggcaccc 540
 aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
 agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
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 gagatcaaa 729

<210> 5

<211> 243
<212> PRT
<213> artificial sequence

<220>
<223> VH2/VL1

<400> 5

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ala Thr Arg Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Gln Lys Leu
50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser
130 135 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Glu Ile Lys

<210> 6
<211> 729
<212> DNA
<213> artificial sequence

<220>
<223> VH2/VL2

<400> 6
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cctggacagg gtctggaatg gattggatac attaataccta gccgtgggtta tactaattac 180
gcacagaagt tgcaggggccg cgtcacaatg actacagaca cttccaccag cacagcctac 240
atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctcttcaggc 360
gaaggtacta gtactgggtc tgggtggaagt ggaggttcag gtggagcaga cgacattgta 420
ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc 480
agagccagtc aaagtgtaag ttacatgaac tggtagcagc agaagccggg caaggcaccc 540
aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaaggtg 720
gagatcaaa 729

<210> 7
<211> 243
<212> PRT
<213> artificial sequence

<220>
<223> VH2/VL2

<400> 7

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ala Thr Arg Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Gln Lys Leu
50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Glu Ile Lys

<210> 8
 <211> 729
 <212> DNA
 <213> artificial sequence

<220>
 <223> VH2/VL3

<400> 8
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 cctggacagg gtctggaatg gattggatac attaatccta gccgtgggta tactaattac 180
 gcacagaagt tgcagggccg cgtcacaatg actacagaca ctccaccag cacagcctac 240
 atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300
 gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc 360
 gaagg tacta gtactgggtc tgggtggaagt ggagggttcag gtggagcaga cgacattgta 420
 ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgacctgc 480
 agagccagtt caagtgtgaa ttacatgaac tgggtaccagc agaagccggg caaggcacc 540
 aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
 agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
 acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaagggtg 720
 gagatcaaa 729

<210> 9
 <211> 243
 <212> PRT
 <213> artificial sequence

<220>
 <223> VH2VL3

<400> 9

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ala Thr Arg Tyr
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Gln Lys Leu
50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys
145 150 155 160

Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Glu Ile Lys

<210> 10
<211> 729

<212> DNA

<213> artificial sequence

<220>

<223> VH3/VL1

<400> 10

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tcctgcaagg cttctggcta caccgctact aggtacacga tgcactgggt aaggcaggca      120
cctggacagg gtctggaatg gattggatac attaatccta gccgtgggtta tactaattac      180
gcacagaagt tgcagggccg cgtcacaatg actacagaca cttccaccag cacagcctac      240
ctgcaaataa acagcctgaa aactgaggac actgcagtct attactgtgc aagatattat      300
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc      360
gaaggtaact gtactgggtc tgggtggaagt ggaggttcag gtggagcaga cgacattcag      420
atgacccagt ctccatctag cctgtctgca tctgtcgggg accgtgtcac catcacctgc      480
agagccagtc aaagtgtaag ttacatgaac tggtagcagc agaagccggg caaggcaccc      540
aaaagatgga tttatgacac atccaaagtg gcttctggag tccttgctcg cttcagtggc      600
agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc      660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaagggtg      720
gagatcaaaa                                     729

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<210> 11

<211> 243

<212> PRT

<213> artificial sequence

<220>

<223> VH3/VL1

<400> 11

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Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1           5           10           15

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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ala Thr Arg Tyr
20           25           30

```

```

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35           40           45

```

```

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Gln Lys Leu
50           55           60

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Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser
130 135 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Glu Ile Lys

<210> 12
<211> 729
<212> DNA
<213> artificial sequence

<220>
<223> VH3/VL2

<400> 12
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cctggacagg gtctggaatg gattggatac attaatccta gccgtgggta tactaattac 180
gcacagaagt tgcagggccg cgtcacaatg actacagaca cttccaccag cacagcctac 240
ctgcaaataga acagcctgaa aactgaggac actgcagtct attactgtgc aagatattat 300
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctcctcaggc 360
gaaggtaact gtactgggtc tgggtggaagt ggagggttcag gtggagcaga cgacattgta 420
ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc 480
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aaaagatgga tttatgacac atccaaagtg gcttctggag tccttgctcg cttcagtggc 600
agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaagggtg 720
gagatcaaaa 729

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<210> 13
<211> 243
<212> PRT
<213> artificial sequence

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<220>
<223> VH3/VL2

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<400> 13

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Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1          5          10          15

```

```

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ala Thr Arg Tyr
          20          25          30

```

```

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
          35          40          45

```

```

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Gln Lys Leu
          50          55          60

```

```

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
          65          70          75          80

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```

Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys
          85          90          95

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Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
 115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
 130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
 145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys

<210> 14
 <211> 729
 <212> DNA
 <213> artificial sequence

<220>
 <223> VH3/VL3

<400> 14
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 cctggacagg gtctggaatg gattggatac attaataccta gccgtgggtta tactaattac 180
 gcacagaagt tgcagggccg cgtcacaatg actacagaca cttccaccag cacagcctac 240
 ctgcaaatga acagcctgaa aactgaggac actgcagtct attactgtgc aagatattat 300

gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcagggc 360
 gaagg tacta gtactgggtc tgggtggaagt ggaggttcag gtggagcaga cgacattgta 420
 ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgacctgc 480
 agagccagtt caagtgtaag ttacatgaac tgggtaccagc agaagccggg caaggcaccc 540
 aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
 agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
 acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaaggtg 720
 gagatcaaa 729

<210> 15
 <211> 243
 <212> PRT
 <213> artificial sequence

<220>
 <223> VH3/VL3

<400> 15

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ala Thr Arg Tyr
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Gln Lys Leu
 50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
 115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
 130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys
 145 150 155 160

Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys

<210> 16
 <211> 729
 <212> DNA
 <213> artificial sequence

<220>
 <223> VH5/VLI

<400> 16
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 cctggacagg gtctggaatg gattggatac attaataccta gccgtgggtta tactaattac 180
 gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 240
 atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300
 gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc 360
 gaaggtaacta gtactgggtc tgggtggaagt ggagggttcag gtggagcaga cgacattcag 420
 atgacccagt ctccatctag cctgtctgca tctgtcgggg accgtgtcac catcacctgc 480
 agagccagtc aaagtgtgaa ttacatgaac tgggtaccagc agaagccggg caaggcacc 540

aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
 agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
 acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaagggtg 720
 gagatcaaa 729

<210> 17
 <211> 243
 <212> PRT
 <213> artificial sequence

<220>
 <223> VH5/VL1

<400> 17

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
 85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
 115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser
 130 135 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
 145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys

<210> 18
 <211> 729
 <212> DNA
 <213> artificial sequence

<220>
 <223> VH5/VL2

<400> 18
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 cctggacagg gtctggaatg gattggatac attaataccta gccgtgggtta tactaattac 180
 gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 240
 atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300
 gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctcctcaggc 360
 gaaggtacta gtactgggtc tgggtggaagt ggaggttcag gtggagcaga cgacattgta 420
 ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc 480
 agagccagtc aaagtgtaag ttacatgaac tgggtaccagc agaagccggg caaggcaccc 540
 aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
 agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
 acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaaggtg 720
 gagatcaaa 729

<210> 19
<211> 243
<212> PRT
<213> artificial sequence

<220>
<223> VH5/VL2

<400> 19

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Glu Ile Lys

<210> 20
<211> 729
<212> DNA
<213> artificial sequence

<220>
<223> VH5/VL3

<400> 20
gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctgggggcctc agtgaagggtg 60
tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 120
cctggacagg gtctggaatg gattggatac attaataccta gccgtgggtta tactaattac 180
gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 240
atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc 360
gaaggtaact gtactgggtc tgggtggaagt ggagggttcag gtggagcaga cgacattgta 420
ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgacctgc 480
agagccagtt caagtgtgta ttacatgaac tgggtaccagc agaagccggg caaggcacc 540
aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaagggtg 720
gagatcaaa 729

<210> 21
<211> 243
<212> PRT
<213> artificial sequence

<220>

<223> VH5/VL3

<400> 21

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys
145 150 155 160

Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys

<210> 22
 <211> 729
 <212> DNA
 <213> artificial sequence

<220>
 <223> VH7/VL1

<400> 22
 gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctgggggcctc agtgaagggtg 60
 tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 120
 cctggacagg gtctggaatg gattggatac attaataccta gccgtgggta tactaattac 180
 aatcagaagt tcaaggaccg cgtcacaaac actacagaca aatccaccag cacagcctac 240
 atggaactga gcagcctgcg ttctgaggac actgcagtct attactgtgc aagatattat 300
 gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctcctcaggc 360
 gaaggtacta gtactgggtc tgggtggaagt ggaggttcag gtggagcaga cgacattcag 420
 atgacccagt ctccatctag cctgtctgca tctgtcgggg accgtgtcac catcacctgc 480
 agagccagtc aaagtgtaag ttacatgaac tgggtaccagc agaagccggg caaggcaccc 540
 aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
 agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
 acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaagggtg 720
 gagatcaaa 729

<210> 23
 <211> 243
 <212> PRT
 <213> artificial sequence

<220>
 <223> VH7/VL1

<400> 23

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser
130 135 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Glu Ile Lys

<210> 24
 <211> 729
 <212> DNA
 <213> artificial sequence

<220>
 <223> VH7/VL2

<400> 24
 gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaagggtg 60
 tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 120
 cctggacagg gtctggaatg gattggatac attaatecta gccgtgggta tactaattac 180
 aatcagaagt tcaaggaccg cgtcacaatc actacagaca aatccaccag cacagcctac 240
 atggaactga gcagcctgcg ttctgaggac actgcagtct attactgtgc aagatattat 300
 gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctcctcaggc 360
 gaagg tacta gtactgggtc tgggtggaagt ggagggttcag gtggagcaga cgacattgta 420
 ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc 480
 agagccagtc aaagtgtgaa ttacatgaac tgggtaccagc agaagccggg caaggcaccc 540
 aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
 agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
 acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaagggtg 720
 gagatcaaa 729

<210> 25
 <211> 243
 <212> PRT
 <213> artificial sequence

<220>
 <223> VH7/VL2

<400> 25

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Glu Ile Lys

<210> 26
<211> 729
<212> DNA
<213> artificial sequence

<220>
<223> VH7/VL3

<400> 26
gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaagggtg 60
tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 120
cctggacagg gtctggaatg gattggatac attaatccta gccgtgggta tactaattac 180
aatcagaagt tcaaggaccg cgtcacaatc actacagaca aatccaccag cacagcctac 240
atggaactga gcagcctgcg ttctgaggac actgcagtct attactgtgc aagatattat 300
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc 360
gaaggtaacta gtactgggtc tgggtggaagt ggaggttcag gtggagcaga cgacattgta 420
ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgacctgc 480
agagccagtt caagtgtaag ttacatgaac tgggtaccagc agaagccggg caaggcacc 540
aaaagatgga tttatgacac atccaaagtg gcttctggag tcctgctcg cttcagtggc 600
agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaagggtg 720
gagatcaaa 729

<210> 27
<211> 243
<212> PRT
<213> artificial sequence

<220>
<223> VH7/VL3

<400> 27

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys
145 150 155 160

Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Glu Ile Lys

<210> 28

<211> 20

<212> DNA

<213> artificial sequence

<220>

<223> Sequencing primer

<400> 28

cctcagacag tggttcaaag

20

<210> 29

<211> 18

<212> DNA

<213> artificial sequence

<220>

<223> Sequencing primer

<400> 29

agccgccacg tgggcctc

18

<210> 30

<211> 1473

<212> DNA

<213> artificial sequence

<220>

<223> anti-CD3 VH5/VL2 x 3-1 VHVL

<400> 30

gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctgggggcctc agtgaaggtg	60
tcttgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca	120
cctggacagg gtctggaatg gattggatac attaataccta gccgtgggtta tactaattac	180
gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac	240
atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat	300
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc	360
gaaggtacta gtactgggtc tgggtggaagt ggaggttcag gtggagcaga cgacattgta	420
ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc	480
agagccagtc aaagtgtaag ttacatgaac tgggtaccagc agaagccggg caaggcaccc	540
aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc	600
agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc	660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaaggtg	720
gagatcaaata ccggaggtgg tggatccgag gtgcagctgc tcgagcagtc tggagctgag	780
ctggtgaaac ctgggggcctc agtgaagata tcttgcaagg cttctggata cgccttcact	840
aactactggc taggttgggt aaagcagagg cctggacatg gacttgagtg gattggagat	900
cttttccctg gaagtggtaa tactcactac aatgagaggt tcaggggcaa agccacactg	960
actgcagaca aatcctcgag cacagccttt atgcagctca gtagcctgac atctgaggac	1020
tctgctgtct atttctgtgc aagattgagg aactgggacg aggctatgga ctactggggc	1080
caagggacca cggtcaccgt ctctcaggt ggtggtggtt ctggcggcgg cggctccggt	1140
ggtggtggtt ctgagctcgt catgaccag tctccatctt atcttgctgc atctcctgga	1200
gaaaccatta ctattaattg cagggaagt aagagcatta gcaaataatt agcctggtat	1260

caagagaaac ctgggaaaac taataagctt cttatctact ctggatccac tttgcaatct 1320
 ggaattccat caaggttcag tggcagtggg tctggtacag atttcactct caccatcagt 1380
 agcctggagc ctgaagattt tgcaatgtat tactgtcaac agcataatga atatccgtac 1440
 acgttcggag gggggaccaa gcttgagatc aaa 1473

<210> 31
 <211> 491
 <212> PRT
 <213> artificial sequence

<220>
 <223> anti-CD3 VH5/VL2 x 3-1 VHVL

<400> 31

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
 85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
 115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
 130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
 145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln
 245 250 255

Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys
 260 265 270

Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Trp Leu Gly Trp Val Lys
 275 280 285

Gln Arg Pro Gly His Gly Leu Glu Trp Ile Gly Asp Leu Phe Pro Gly
 290 295 300

Ser Gly Asn Thr His Tyr Asn Glu Arg Phe Arg Gly Lys Ala Thr Leu
 305 310 315 320

Thr Ala Asp Lys Ser Ser Ser Thr Ala Phe Met Gln Leu Ser Ser Leu
 325 330 335

Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Leu Arg Asn Trp
 340 345 350

Asp Glu Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser
 355 360 365

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 370 375 380

Glu Leu Val Met Thr Gln Ser Pro Ser Tyr Leu Ala Ala Ser Pro Gly
 385 390 395 400

Glu Thr Ile Thr Ile Asn Cys Arg Ala Ser Lys Ser Ile Ser Lys Tyr
 405 410 415

Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Thr Asn Lys Leu Leu Ile
 420 425 430

Tyr Ser Gly Ser Thr Leu Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly
 435 440 445

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
 450 455 460

Glu Asp Phe Ala Met Tyr Tyr Cys Gln Gln His Asn Glu Tyr Pro Tyr
 465 470 475 480

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 485 490

<210> 32

<211> 1500

<212> DNA

<213> artificial sequence

<220>

<223> anti-CD3 VH5/VL2 x 4-7 VHVL

<400> 32

gacgtccaac tggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaagggtg 60

tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 120

cctggacagg gtctggaatg gattggatac attaatccta gccgtgggta tactaattac 180

gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 240

atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300

gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctcctcaggc 360

gaaggtaacta gtactgggtc tggtggaagt ggagggttcag gtggagcaga cgacattgta 420

ctgaccagct ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc 480

agagccagtc aaagtgtgtaag ttacatgaac tggtaccagc agaagccggg caaggcaccc 540

aaaagatgga tttatgacac atccaaagtg gcttctggag tccttgctcg cttcagtggc 600

agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660

acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaagggtg 720

gagatcaa at ccggagggtg tggatccgag gtgcagctgc tcgagcagtc tggagctgag 780
 ctggcgaggc ctggggcttc agtgaagctg tcctgcaagg cttctggcta caccttcaca 840
 aactatgggt taagctgggt gaagcagagg cctggacagg tccttgagtg gattggagag 900
 gtttatccta gaattggtaa tgcttactac aatgagaagt tcaagggcaa ggccacactg 960
 actgcagaca aatcctccag cacagcgtcc atggagctcc gcagcctgac ctctgaggac 1020
 tctgcggtct atttctgtgc aagacgggga tcctacgata ctaactacga ctggtacttc 1080
 gatgtctggg gccaaaggac cacggtcacc gtctcctcag gtgggtgggtg ttctggcggc 1140
 ggcggctccg gtgggtgggtg ttctgagctc gtgatgacct agactccact ctccctgcct 1200
 gtcagtcttg gagatcaagc ctccatctct tgcagatcta gtcagagcct tgtacacagt 1260
 aatggaaaca cctatttaca ttggtacctg cagaagccag gccagtctcc aaagctcctg 1320
 atctacaaag tttccaaccg attttctggg gtcccagaca ggttcagtgg cagtggatca 1380
 gggacagatt tcacactcaa gatcagcaga gtggaggctg aggatctggg agtttatttc 1440
 tgctctcaaa gtacacatgt tccgtacacg ttcggagggg ggaccaagct tgagatcaaa 1500

<210> 33

<211> 500

<212> PRT

<213> artificial sequence

<220>

<223> anti-CD3 VH5/VL2 x 4-7 VHVL

<400> 33

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
 85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln
245 250 255

Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys
260 265 270

Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys
275 280 285

Gln Arg Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg
290 295 300

Ile Gly Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu
305 310 315 320

Thr Ala Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu

325

330

335

Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr
 340 345 350

Asp Thr Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr
 355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 370 375 380

Gly Gly Gly Ser Glu Leu Val Met Thr Gln Thr Pro Leu Ser Leu Pro
 385 390 395 400

Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
 405 410 415

Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys
 420 425 430

Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe
 435 440 445

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
 450 455 460

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe
 465 470 475 480

Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys
 485 490 495

Leu Glu Ile Lys
 500

<210> 34
 <211> 1500
 <212> DNA
 <213> artificial sequence

<220>
 <223> anti-CD3 VH5/VL2 x 4-7 VLVH

<400> 34
 gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaagggtg 60
 tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 120

cctggacagg gtctggaatg gattggatac attaatccta gccgtgggtta tactaattac 180
gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 240
atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctcctcaggc 360
gaaggtacta gtactgggtc tgggtggaagt ggaggttcag gtggagcaga cgacattgta 420
ctgacccagt ctcagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc 480
agagccagtc aaagtgtaag ttacatgaac tgggtaccagc agaagccggg caaggcaccc 540
aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaagggtg 720
gagatcaaat ccggagggtg tggatccgag ctctgatga cccagactcc actctccctg 780
cctgtcagtc ttggagatca agcctccatc tcttgagat ctagtcagag ccttgtagac 840
agtaatggaa acacctatctt acattggtac ctgcagaagc caggccagtc tccaaagctc 900
ctgatctaca aagtttccaa ccgattttct ggggtcccag acaggttcag tggcagtgga 960
tcagggacag atttcacact caagatcagc agagtggagg ctgaggatct gggagtttat 1020
ttctgctctc aaagtacaca tggtccgtac acgttcggag gggggaccaa gcttgagatc 1080
aaaggtggtg gtggttctgg cggcggcggc tccggtggtg gtggttctga ggtgcagctg 1140
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gcttctggct acaccttcac aaactatggt ttaagctggg tgaagcagag gcctggacag 1260
gtccttgagt ggattggaga ggtttatcct agaattggta atgcttacta caatgagaag 1320
ttcaagggca aggccacact gactgcagac aaatcctcca gcacagcgtc catggagctc 1380
cgcagcctga cctctgagga ctctgcggtc tatttctgtg caagacgggg atcctacgat 1440
actaactacg actggtactt cgatgtctgg ggccaaggga ccacggtcac cgtctcctca 1500

<210> 35

<211> 500

<212> PRT

<213> artificial sequence

<220>

<223> anti-CD3 VH5/VL2 x 4-7 VLVH

<400> 35

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala

1	5	10	15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr	20	25	30
Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile	35	40	45
Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val	50	55	60
Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr	65	70	75
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys	85	90	95
Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly	100	105	110
Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly	115	120	125
Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser	130	135	140
Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys	145	150	155
Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro	165	170	175
Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser	180	185	190
Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser	195	200	205
Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys	210	215	220
Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val	225	230	235
			240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Thr
 245 250 255

Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys
 260 265 270

Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His
 275 280 285

Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys
 290 295 300

Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
 305 310 315 320

Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp
 325 330 335

Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe
 340 345 350

Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly
 355 360 365

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln Ser
 370 375 380

Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys Lys
 385 390 395 400

Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys Gln
 405 410 415

Arg Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg Ile
 420 425 430

Gly Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr
 435 440 445

Ala Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr
 450 455 460

Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr Asp
 465 470 475 480

Thr Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val
 485 490 495

Thr Val Ser Ser
 500

<210> 36

<211> 1491

<212> DNA

<213> artificial sequence

<220>

<223> anti-CD3 VH5/VL2 x 5-10 VHVL

<400> 36

gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaagggtg	60
tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca	120
cctggacagg gtctggaatg gattggatac attaatccta gccgtgggtta tactaattac	180
gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac	240
atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat	300
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc	360
gaaggtaacta gtactgggtc tgggtggaagt ggagggttcag gtggagcaga cgacattgta	420
ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc	480
agagccagtc aaagtgtgag ttacatgaac tgggtaccagc agaagccggg caaggcaccc	540
aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc	600
agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc	660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcgggtggcg gaccaagggtg	720
gagatcaaact ccggagggtg tggatccgag gtgcagctgc tcgagcagtc tggagctgag	780
ctggtaaggc ctgggacttc agtgaagata tcctgcaagg cttctggata cgccttcact	840
aactactggc taggttgggt aaagcagagg cctggacatg gacttgagtg gattggagat	900
attttccctg gaagtggtaa tatccactac aatgagaagt tcaagggcaa agccacactg	960
actgcagaca aatcttcgag cacagcctat atgcagctca gtagcctgac atttgaggac	1020
tctgctgtct atttctgtgc aagactgagg aactgggacg agcctatgga ctactggggc	1080
caagggacca cggtcaccgt ctctcagggt ggtggtggtt ctggcggcgg cggctccggt	1140
ggtggtggtt ctgagctcgt gatgacacag tctccatcct ccctgactgt gacagcagga	1200
gagaagggtca ctatgagctg caagtccagt cagagtctgt taaacagtgg aaatcaaaag	1260

aactacttga cctggtacca gcagaaacca gggcagcctc ctaaactgtt gatctactgg 1320
 gcatccacta ggggaatctgg ggtccctgat cgcttcacag gcagtggatc tggaacagat 1380
 ttcactctca ccatcagcag tgtgcaggct gaagacctgg cagtttatta ctgtcagaat 1440
 gattatagtt atccgctcac gttcgggtgct gggaccaagc ttgagatcaa a 1491

<210> 37
 <211> 497
 <212> PRT
 <213> artificial sequence

<220>
 <223> anti-CD3 VH5/VL2 x 5-10 VHVL

<400> 37

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
 85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
 115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
 130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
 145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln
 245 250 255

Ser Gly Ala Glu Leu Val Arg Pro Gly Thr Ser Val Lys Ile Ser Cys
 260 265 270

Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Trp Leu Gly Trp Val Lys
 275 280 285

Gln Arg Pro Gly His Gly Leu Glu Trp Ile Gly Asp Ile Phe Pro Gly
 290 295 300

Ser Gly Asn Ile His Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu
 305 310 315 320

Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu
 325 330 335

Thr Phe Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Leu Arg Asn Trp
 340 345 350

Asp Glu Pro Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser
 355 360 365

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 370 375 380

Glu Leu Val Met Thr Gln Ser Pro Ser Ser Leu Thr Val Thr Ala Gly
 385 390 395 400

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
 405 410 415

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
 420 425 430

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 435 440 445

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 450 455 460

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Asn
 465 470 475 480

Asp Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile
 485 490 495

Lys

<210> 38
 <211> 1491
 <212> DNA
 <213> artificial sequence

<220>
 <223> anti-CD3 VH5/VL2 x 5-10 VLVH

<400> 38
 gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaagggtg 60
 tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 120
 cctggacagg gtctggaatg gattggatac attaatccta gccgtgggta tactaattac 180
 gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 240
 atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300
 gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctccctcaggc 360
 gaagg tacta gtactgggtc tgggtggaagt ggaggttcag gtggagcaga cgacattgta 420
 ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc 480
 agagccagtc aaagtgtaag ttacatgaac tggtagcagc agaagccggg caaggcaccc 540
 aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600

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agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaaggtg 720
gagatcaaat ccggaggtgg tggatccgag ctctgatga cacagtctcc atcctccctg 780
actgtgacag caggagagaa ggtcactatg agctgcaagt ccagtcagag tctgttaaac 840
agtggaaatc aaaagaacta cttgacctgg taccagcaga aaccagggca gcctcctaaa 900
ctgttgatct actgggcata cactagggaa tctgggggtcc ctgatcgctt cacaggcagt 960
ggatctggaa cagatttcac tctcaccatc agcagtgtgc aggctgaaga cctggcagtt 1020
tattactgtc agaatgatta tagttatccg ctacagttcg gtgctgggac caagcttgag 1080
atcaaaggtg gtggtgggtc tggcggcggc ggctccggtg gtggtgggtc tgaggtgcag 1140
ctgctcgagc agtctggagc tgagctggta aggctggga cttcagtgaa gatatcctgc 1200
aaggcttctg gatacgctt cactaactac tggctaggtt gggtaaagca gaggcctgga 1260
catggacttg agtggattgg agatattttc cctggaagtg gtaatatcca ctacaatgag 1320
aagttcaagg gcaaagccac actgactgca gacaaatctt cgagcacagc ctatatgcag 1380
ctcagtagcc tgacatttga ggactctgct gtctatttct gtgcaagact gaggaactgg 1440
gacgagccta tggactactg gggccaaggg accacgggtc ccgtctctc a 1491

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<210> 39

<211> 497

<212> PRT

<213> artificial sequence

<220>

<223> anti-CD3 VH5/VL2 x 5-10 VLVH

<400> 39

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Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1           5           10           15

```

```

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20           25           30

```

```

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35           40           45

```

```

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
50           55           60

```

```

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
65           70           75           80

```

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Ser
245 250 255

Pro Ser Ser Leu Thr Val Thr Ala Gly Glu Lys Val Thr Met Ser Cys
260 265 270

Lys Ser Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu
275 280 285

Thr Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
290 295 300

Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser

305 310 315 320
 Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu
 325 330 335
 Asp Leu Ala Val Tyr Tyr Cys Gln Asn Asp Tyr Ser Tyr Pro Leu Thr
 340 345 350
 Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly
 355 360 365
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln
 370 375 380
 Ser Gly Ala Glu Leu Val Arg Pro Gly Thr Ser Val Lys Ile Ser Cys
 385 390 395 400
 Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Trp Leu Gly Trp Val Lys
 405 410 415
 Gln Arg Pro Gly His Gly Leu Glu Trp Ile Gly Asp Ile Phe Pro Gly
 420 425 430
 Ser Gly Asn Ile His Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu
 435 440 445
 Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu
 450 455 460
 Thr Phe Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Leu Arg Asn Trp
 465 470 475 480
 Asp Glu Pro Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser
 485 490 495

Ser

<210> 40
 <211> 35
 <212> DNA
 <213> artificial sequence
 <220>
 <223> DI anti-CD3 K52VHBsrGI

<400> 40
aggtgtacac tccgacgtcc aactgggtgca gtcag

35

<210> 41
<211> 30
<212> DNA
<213> artificial sequence

<220>
<223> DI anti-CD3 52VLBspEI

<400> 41
aatccggatt tgatctccac cttgggtcccg

30

<210> 42
<211> 51
<212> DNA
<213> artificial sequence

<220>
<223> 4-7 VH GS15 FOR

<400> 42
ggcggcggcg gctccggtgg tgggtggttct gaggtgcagc tgctcgagca g

51

<210> 43
<211> 53
<212> DNA
<213> artificial sequence

<220>
<223> 4-7 VH SalI REV

<400> 43
ttttaagtgcg acctaatgat gatgatgatg atgtgaggag acggtgaccg tgg

53

<210> 44
<211> 49
<212> DNA
<213> artificial sequence

<220>
<223> 510VLBspEI

<400> 44
ctgaaatccg gaggtggtgg atccgagctc gtgatgacac agtctccat

49

<210> 45
<211> 53
<212> DNA
<213> artificial sequence

<220>
<223> 510VLGS15REV

<400> 45
ggagccgccg ccgccagaac caccaccacc ttgatctca agcttggtcc cag 53

<210> 46
<211> 49
<212> DNA
<213> artificial sequence

<220>
<223> 510VHGS15

<400> 46
ggcggcgccg gctccggtgg tgggtggttct gaggtgcagc tgctcgagc 49

<210> 47
<211> 53
<212> DNA
<213> artificial sequence

<220>
<223> 510VHSalIREV

<400> 47
ttttaagtcg acctaagat gatgatgatg atgtgaggag acggtgaccg tgg 53

<210> 48
<211> 1518
<212> DNA
<213> artificial sequence

<220>
<223> 3-1(VL-VH)xanti-CD3(VH(5)-VL(2))

<400> 48
atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacaggtgt acactccgag 60
ctcgatcatga ccagtcctcc atcttatctt gctgcatctc ctggagaaac cattactatt 120
aattgcaggg caagtaagag cattagcaaa tatttagcct ggtatcaaga gaaacctggg 180
aaaactaata agcttcttat ctactctgga tccactttgc aatctggaat tccatcaagg 240
ttcagtggca gtggatctgg tacagatttc actctcacca tcagtagcct ggagcctgaa 300
gattttgcaa tgtattactg tcaacagcat aatgaatatc cgtacacgtt cggagggggg 360
accaagcttg agatcaaagg tgggtggtggt tctggcgccg gcggctccgg tgggtggtggt 420
tctgaggtgc agctgctcga gcagtctgga gctgagctgg tgaaacctgg ggcctcagtg 480
aagatatcct gcaaggcttc tggatacgcc ttcactaact actggctagg ttgggtaaag 540
cagaggcctg gacatggact tgagtggatt ggagatcttt tccttggaag tggtataact 600
cactacaatg agaggttcag gggcaaagcc acactgactg cagacaaatc ctcgagcaca 660

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gcctttatgc agctcagtag cctgacatct gaggactctg ctgtctattt ctgtgcaaga 720
ttgaggaact gggacgaggc tatggactac tggggccaag ggaccacggt caccgtctcc 780
tccggaggtg gtggctccga cgtccaactg gtgcagtcag gggctgaagt gaaaaaacct 840
ggggcctcag tgaaggtgtc ctgcaaggct tctggctaca cttttactag gtacacgatg 900
cactgggtaa ggcaggcacc tggacagggt ctggaatgga ttggatacat taatcctagc 960
cgtgggtata ctaattacgc agacagcgtc aagggccgct tcacaatcac tacagacaaa 1020
tccaccagca cagcctacat ggaactgagc agcctgcgtt ctgaggacac tgcaacctat 1080
tactgtgcaa gatattatga tgatcattac tgccttgact actggggcca aggcaccacg 1140
gtcaccgtct cctcaggcga aggtactagt actggttctg gaggttcagg tggagcagac 1200
gacattgtac tgacccagtc tccagcaact ctgtctctgt ctccagggga gcgtgccacc 1260
ctgagctgca gagccagtca aagtgtaagt tacatgaact ggtaccagca gaagccgggc 1320
aaggcaccca aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctcgc 1380
ttcagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa 1440
gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cggtggcggg 1500
accaaggtgg agatcaaa 1518

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```

<210> 49
<211> 506
<212> PRT
<213> artificial sequence

```

```

<220>
<223> 3-1(VL-VH)xanti-CD3(VH(5)-VL(2))

```

```

<400> 49

```

```

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1           5           10           15

```

```

Val His Ser Glu Leu Val Met Thr Gln Ser Pro Ser Tyr Leu Ala Ala
20           25           30

```

```

Ser Pro Gly Glu Thr Ile Thr Ile Asn Cys Arg Ala Ser Lys Ser Ile
35           40           45

```

```

Ser Lys Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Thr Asn Lys
50           55           60

```

```

Leu Leu Ile Tyr Ser Gly Ser Thr Leu Gln Ser Gly Ile Pro Ser Arg

```

65		70		75		80
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser						
		85		90		95
Leu Glu Pro Glu Asp Phe Ala Met Tyr Tyr Cys Gln Gln His Asn Glu						
		100		105		110
Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly						
		115		120		125
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln						
		130		135		140
Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val						
		145		150		155
Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Trp Leu						
		165		170		175
Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp Ile Gly Asp						
		180		185		190
Leu Phe Pro Gly Ser Gly Asn Thr His Tyr Asn Glu Arg Phe Arg Gly						
		195		200		205
Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Phe Met Gln						
		210		215		220
Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg						
		225		230		235
Leu Arg Asn Trp Asp Glu Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr						
		245		250		255
Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Val Gln Leu Val Gln						
		260		265		270
Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys						
		275		280		285
Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg						
		290		295		300

Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser
305 310 315 320

Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile
325 330 335

Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu
340 345 350

Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp
355 360 365

His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser
370 375 380

Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser Gly Gly Ala Asp
385 390 395 400

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
405 410 415

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
420 425 430

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
435 440 445

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
450 455 460

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
465 470 475 480

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
485 490 495

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
500 505

<210> 50

<211> 60

<212> DNA

<213> artificial sequence

<220>

<223> Me83

<400> 50
ggttctggcg gcggcggctc cggtggtggt ggttctgagg tgcagctgct cgacagtctg 60

<210> 51
<211> 41
<212> DNA
<213> artificial sequence

<220>
<223> Me84

<400> 51
gtgctccgga ggagacggtg accgtggtcc cttggcccca g 41

<210> 52
<211> 53
<212> DNA
<213> artificial sequence

<220>
<223> Me90

<400> 52
ccggagccgc cgccgccaga accaccacca cctttgatct caagcttggt ccc 53

<210> 53
<211> 52
<212> DNA
<213> artificial sequence

<220>
<223> Me91a

<400> 53
ggattgtaca ctccgagctc gtcattgacc agtctccatc ttatcttgct gc 52

<210> 54
<211> 1560
<212> DNA
<213> artificial sequence

<220>
<223> 3-5(VL-VH)xanti-CD3 (VH(5)-VL(2))

<400> 54
atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacaggtgt acactccgcg 60
cgcgagctcg tgatgacca gactccactc tccctgcctg tcagtcttgg agatcaagcc 120
tccatctctt gcagatctag tcagagcctt gtacacagta atggaaacac ctatttacat 180
tggtacctgc agaagccagg ccagtctcca aagctcctga tctacaaagt ttccaaccga 240
ttttctgggg tcccagacag gttcagtggc agtggatcag ggacagattt cacactcaag 300

atcagcagag tggaggctga ggatctggga gtttatttct gctctcaaag tacacatgtt 360
 ccgtacacgt tcggaggggg gaccaagctt gagatcaaag gtggtggtgg ttctggcggc 420
 ggcggctccg gtggtggtgg ttctgaggtg cagctgctcg agcagtctgg agctgagctg 480
 gtaaggcctg ggacttcagt gaagctgtcc tgcaaggctt ctggctacac cttcacaagc 540
 tatggtttaa gctgggtgaa gcagagaact ggacagggcc ttgagtggat tggagaggtt 600
 taccctagaa ttggtaatgc ttactacaat gagaagttca agggcaaggc cacactgact 660
 gcagacaaat cctccagcac agcgtccatg gagctccgca gcctgacatc tgaggactct 720
 gcggtctatt tctgtgcaag acgggggatcc tacggtagta actacgactg gtacttcgat 780
 gtctggggcc aagggaaccac ggtcaccgtc tctccggag gtggtggctc cgacgtccaa 840
 ctggtgcagt caggggctga agtgaaaaaa cctggggcct cagtgaagggt gtcctgcaag 900
 gcttctggct acacctttac taggtacacg atgcactggg taaggcaggc acctggacag 960
 ggtctggaat ggattggata cattaatcct agccgtgggt atactaatta cgcagacagc 1020
 gtcaagggcc gcttcacaat cactacagac aaatccacca gcacagccta catggaactg 1080
 agcagcctgc gttctgagga cactgcaacc tattactgtg caagatatta tgatgatcat 1140
 tactgccttg actactgggg ccaaggcacc acggtcaccg tctcctcagg cgaagggtact 1200
 agtactgggt ctggtggaag tggaggttca ggtggagcag acgacattgt actgaccag 1260
 tctccagcaa ctctgtctct gtctccaggg gagcgtgcc aacctgagctg cagagccagt 1320
 caaagtgtaa gttacatgaa ctggtaccag cagaagccgg gcaaggcacc caaaagatgg 1380
 atttatgaca catccaaagt ggcttctgga gtccctgctc gcttcagtgg cagtgggtct 1440
 gggaccgact actctctcac aatcaacagc ttggaggctg aagatgctgc cacttattac 1500
 tgccaacagt ggagtagtaa cccgctcacg ttcggtggcg ggaccaagggt ggagatcaaa 1560

<210> 55

<211> 520

<212> PRT

<213> artificial sequence

<220>

<223> 3-5(VL-VH)xanti-CD3 (VH(5)-VL(2))

<400> 55

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1 5 10 15

Val His Ser Ala Arg Glu Leu Val Met Thr Gln Thr Pro Leu Ser Leu

20

25

30

Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln
 35 40 45

Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln
 50 55 60

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg
 65 70 75 80

Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
 85 90 95

Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr
 100 105 110

Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr
 115 120 125

Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 130 135 140

Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu
 145 150 155 160

Val Arg Pro Gly Thr Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr
 165 170 175

Thr Phe Thr Ser Tyr Gly Leu Ser Trp Val Lys Gln Arg Thr Gly Gln
 180 185 190

Gly Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg Ile Gly Asn Ala Tyr
 195 200 205

Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser
 210 215 220

Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser
 225 230 235 240

Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr Gly Ser Asn Tyr Asp
 245 250 255

Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
260 265 270

Gly Gly Gly Gly Ser Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val
275 280 285

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
290 295 300

Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln Ala Pro Gly Gln
305 310 315 320

Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn
325 330 335

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser
340 345 350

Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
355 360 365

Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp
370 375 380

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr
385 390 395 400

Ser Thr Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile
405 410 415

Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg
420 425 430

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp
435 440 445

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr
450 455 460

Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser
465 470 475 480

Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala
485 490 495

Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly
500 505 510

Gly Gly Thr Lys Val Glu Ile Lys
515 520

<210> 56
<211> 40
<212> DNA
<213> artificial sequence

<220>
<223> Me81

<400> 56
ggatgcgcgc gagctcgtga tgaccagac tccactctcc 40

<210> 57
<211> 1545
<212> DNA
<213> artificial sequence

<220>
<223> 4-1(VL-VH)xanti-CD3(VH(5)-VL(2)).

<400> 57
atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacaggtgt acactccgag 60
ctcgtgatga cacagtctcc atcctccctg agtgtgtcag caggagagaa ggtcactatg 120
agctgcaagt ccagtcagag tctgttaaac agtggaatc aaaagaacta cttggcctgg 180
taccagcaga aaccagggca gcctcctaaa ctgttgatct acggggcatt cactagggaa 240
tctgggggtcc ctgatcgctt cacaggcagt ggatctggaa cagatttcac tctcaccatc 300
agcagtgtgc aggctgaaga cctggcagtt tattactgtc agaatgatta tagttatccg 360
tacacgttcg gaggggggac caagcttgag atcaaagggtg gtggtggttc tggcggcggc 420
ggctccgggtg gtggtggttc tgagggtgcag ctgctcgagc agtctggagc tgagctggta 480
aggcctggga cttcagtga gatatactgc aaggcttctg gatacgcctt cactaactac 540
tggttaggtt ggggttaagca gaggcctgga catggacttg aatgggttgg agatattttc 600
cctggaagtg gtaatgctca ctacaatgag aagttcaagg gcaaagccac actgactgca 660
gacaagtcct cgtacacagc ctatatgcag ctcagtagcc tgacatctga ggactctgct 720
gtctattttct gtgcaagatt gcggaactgg gacgaggcta tggactactg gggccaaggg 780
accacggtca ccgtctcttc cggaggtggg ggctccgacg tccaactggg gcagtcaggg 840
gctgaagtga aaaaacctgg ggcctcagtg aaggtgtcct gcaaggcttc tggctacacc 900

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tttactaggt acacgatgca ctgggtaagg caggcacctg gacaggggtct ggaatggatt 960
ggatacatta atcctagccg tggttataact aattacgcag acagcgtcaa gggccgcttc 1020
acaatcacta cagacaaatc caccagcaca gcctacatgg aactgagcag cctgcgttct 1080
gaggacactg caacctatta ctgtgcaaga tattatgatg atcattactg ccttgactac 1140
tggggccaag gcaccacggt caccgtctcc tcaggcgaag gtactagtagt tggttctggg 1200
ggaagtggag gttcagggtg agcagacgac attgtactga ccaggtctcc agcaactctg 1260
tctctgtctc caggggagcg tgccaccctg agctgcagag ccagtcaaag tgtaagttac 1320
atgaactggg accagcagaa gccgggcaag gcacccaaaa gatggattta tgacacatcc 1380
aaagtggctt ctggagtccc tgctcgcttc agtggcagtg ggtctgggac cgactactct 1440
ctcacaatca acagcttgga ggctgaagat gctgccactt attactgcca acagtggagt 1500
agtaaccgcg tcacgttcgg tggcgggacc aaggtggaga tcaaa 1545

```

<210> 58

<211> 515

<212> PRT

<213> artificial sequence

<220>

<223> 4-1(VL-VH)xanti-CD3(VH(5)-VL(2))

<400> 58

```

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1           5           10           15

```

```

Val His Ser Glu Leu Val Met Thr Gln Ser Pro Ser Ser Leu Ser Val
          20           25           30

```

```

Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu
          35           40           45

```

```

Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys
50           55           60

```

```

Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Gly Ala Ser Thr Arg Glu
65           70           75           80

```

```

Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe
          85           90           95

```

```

Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr

```

100					105					110					
Cys	Gln	Asn	Asp	Tyr	Ser	Tyr	Pro	Tyr	Thr	Phe	Gly	Gly	Gly	Thr	Lys
		115					120					125			
Leu	Glu	Ile	Lys	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly
	130					135					140				
Gly	Gly	Ser	Glu	Val	Gln	Leu	Leu	Glu	Gln	Ser	Gly	Ala	Glu	Leu	Val
145					150					155					160
Arg	Pro	Gly	Thr	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ala
				165					170					175	
Phe	Thr	Asn	Tyr	Trp	Leu	Gly	Trp	Val	Lys	Gln	Arg	Pro	Gly	His	Gly
			180					185					190		
Leu	Glu	Trp	Val	Gly	Asp	Ile	Phe	Pro	Gly	Ser	Gly	Asn	Ala	His	Tyr
		195					200					205			
Asn	Glu	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	Ser	Ser
	210					215					220				
Tyr	Thr	Ala	Tyr	Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala
225					230					235					240
Val	Tyr	Phe	Cys	Ala	Arg	Leu	Arg	Asn	Trp	Asp	Glu	Ala	Met	Asp	Tyr
				245					250					255	
Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser
			260					265					270		
Asp	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala
		275					280					285			
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Arg	Tyr
	290					295					300				
Thr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile
305					310					315					320
Gly	Tyr	Ile	Asn	Pro	Ser	Arg	Gly	Tyr	Thr	Asn	Tyr	Ala	Asp	Ser	Val
				325					330					335	

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
 340 345 350

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
 355 360 365

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 370 375 380

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
 385 390 395 400

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
 405 410 415

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
 420 425 430

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 435 440 445

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 450 455 460

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 465 470 475 480

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 485 490 495

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 500 505 510

Glu Ile Lys
 515

<210> 59
 <211> 44
 <212> DNA
 <213> artificial sequence

<220>
 <223> Me92a

<400> 59
 ggattgtaca ctccgagctc gtgatgacac agtctccatc ctcc

<210> 60
<211> 1560
<212> DNA
<213> artificial sequence

<220>
<223> 4-7 (VL-VH) xanti-CD3 (VH(5)-VL(2))

<400> 60
atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacaggtgt acactccgcg 60
cgcgagctcg tgatgaccca gactccactc tccctgcctg tcagtcttgg agatcaagcc 120
tccatctctt gcagatctag tcagagcctt gtacacagta atggaaacac ctatttacat 180
tggtacctgc agaagccagg ccagtctcca aagctcctga tctacaaagt ttccaaccga 240
ttttctgggg tcccagacag gttcagtggc agtggatcag ggacagattt cacactcaag 300
atcagcagag tggaggctga ggatctggga gtttatttct gctctcaaag tacacatgtt 360
ccgtacacgt tcggaggggg gaccaagctt gagatcaaag gtggtggtgg ttctggcggc 420
ggcggctccg gtggtggtgg ttctgaggtg cagctgctcg agcagtctgg agctgagctg 480
gcgaggcctg gggcttcagt gaagctgtcc tgcaaggctt ctggctacac cttcacaac 540
tatggtttaa gctgggtgaa gcagaggcct ggacaggctc ttgagtggat tggagagggt 600
tatcctagaa ttggtaatgc ttactacaat gagaagttca agggcaaggc cacactgact 660
gcagacaaat cctccagcac agcgtccatg gagctccgca gcctgacctc tgaggactct 720
gcggtctatt tctgtgcaag acgggggatcc tacgatacta actacgactg gtacttcgat 780
gtctggggcc aagggaccac ggtcaccgtc tcctccggag gtggtggctc cgacgtccaa 840
ctggtgcagt caggggctga agtgaaaaaa cctggggcct cagtgaagggt gtcctgcaag 900
gcttctgggt acacctttac taggtacacg atgcactggg taaggcaggc acctggacag 960
ggtctggaat ggattggata cattaatcct agccgtgggt atactaatta cgcagacagc 1020
gtcaagggcc gcttcacaat cactacagac aaatccacca gcacagccta catggaactg 1080
agcagcctgc gttctgagga cactgcaacc tattactgtg caagatatta tgatgatcat 1140
tactgccttg actactgggg ccaaggcacc acggtcaccg tctcctcagg cgaagggtact 1200
agtactgggt ctggtggaag tggagggtca ggtggagcag acgacattgt actgaccag 1260
tctccagcaa ctctgtctct gtctccaggg gagcgtgcca ccctgagctg cagagccagt 1320
caaagtgtaa gttacatgaa ctggtaccag cagaagccgg gcaaggcacc caaaagatgg 1380
atztatgaca catccaaagt ggcttctgga gtcctgctc gcttcagtgg cagtgggtct 1440
gggaccgact actctctcac aatcaacagc ttggaggctg aagatgctgc cacttattac 1500

tgccaacagt ggagtagtaa cccgctcacg ttcgggtggcg ggaccaaggt ggagatcaaa 1560

<210> 61

<211> 520

<212> PRT

<213> artificial sequence

<220>

<223> 4-7(VL-VH)xanti-CD3(VH(5)-VL(2))

<400> 61

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser Ala Arg Glu Leu Val Met Thr Gln Thr Pro Leu Ser Leu
20 25 30

Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln
35 40 45

Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln
50 55 60

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg
65 70 75 80

Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
85 90 95

Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr
100 105 110

Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr
115 120 125

Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
130 135 140

Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu
145 150 155 160

Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr
165 170 175

Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys Gln Arg Pro Gly Gln

180

185

190

Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg Ile Gly Asn Ala Tyr
195 200 205

Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser
210 215 220

Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser
225 230 235 240

Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr Asp Thr Asn Tyr Asp
245 250 255

Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
260 265 270

Gly Gly Gly Gly Ser Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val
275 280 285

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
290 295 300

Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln Ala Pro Gly Gln
305 310 315 320

Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn
325 330 335

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser
340 345 350

Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
355 360 365

Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp
370 375 380

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr
385 390 395 400

Ser Thr Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile
405 410 415

Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg
 420 425 430

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp
 435 440 445

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr
 450 455 460

Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser
 465 470 475 480

Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala
 485 490 495

Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly
 500 505 510

Gly Gly Thr Lys Val Glu Ile Lys
 515 520

<210> 62

<211> 1545

<212> DNA

<213> artificial sequence

<220>

<223> 5-10 (VL-VH)xanti-CD3 (VH(5)-VL(2))

<400> 62

atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacaggtgt aactccgag 60

ctcgtgatga cacagtctcc atcctccctg actgtgacag caggagagaa ggtcactatg 120

agctgcaagt ccagtcagag tctgttaaag agtggaatc aaaagaacta cttgacctgg 180

taccagcaga aaccagggca gcctcctaaa ctgttgatct actgggcac cactagggaa 240

tctgggggtcc ctgatcgctt cacaggcagt ggatctggaa cagatttcac tctcaccatc 300

agcagtgtgc aggctgaaga cctggcagtt tattactgtc agaatgatta tagttatccg 360

ctcacgttcg gtgctgggac caagcttgag atcaaaggtg gtggtggttc tggcggcggc 420

ggctccggtg gtggtggttc tgagggtgcag ctgctcgagc agtctggagc tgagctggta 480

aggcctggga cttcagtgaa gatatcctgc aaggcttctg gatacgctt cactaactac 540

tggctagggtt gggtaaagca gaggcctgga catggacttg agtggattgg agatattttc 600

cctggaagtg gtaatatcca ctacaatgag aagttcaagg gcaaagccac actgactgca 660

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gacaaatctt cgagcacagc ctatatgcag cttagtagcc tgacatttga ggactctgct 720
gtctatttct gtgcaagact gaggaactgg gacgagccta tggactactg gggccaaggg 780
accacggtca ccgtctcctc cggaggtggg ggctccgacg tccaactggg gcagtcaggg 840
gctgaagtga aaaaacctgg ggcctcagtg aaggtgtcct gcaaggcttc tggctacacc 900
tttactaggt acacgatgca ctgggtaagg caggcacctg gacaggggtct ggaatggatt 960
ggatacatta atcctagccg tggttatact aattacgcag acagcgtcaa gggccgcttc 1020
acaatcacta cagacaaatc caccagcaca gcctacatgg aactgagcag cctgcgttct 1080
gaggacactg caacctatta ctgtgcaaga tattatgatg atcattactg ccttgactac 1140
tgggggccaag gcaccacggg caccgtctcc tcaggcgaag gtactagtagc tggttctggg 1200
ggaagtggag gttcaggtgg agcagacgac attgtactga ccaggtctcc agcaactctg 1260
tctctgtctc caggggagcg tgccaccctg agctgcagag ccagtcaaag tgtaagttac 1320
atgaactggg accagcagaa gccgggcaag gcacccaaaa gatggattta tgacacatcc 1380
aaagtggctt ctggagtccc tgctcgcttc agtggcagtg ggtctgggac cgactactct 1440
ctcacaatca acagcttgga ggctgaagat gctgccactt attactgcca acagtggagt 1500
agtaaccgcg tcacgttcgg tggcgggacc aaggtggaga tcaaa 1545

```

<210> 63

<211> 515

<212> PRT

<213> artificial sequence

<220>

<223> 5-10 (VL-VH) xanti-CD3 (VH(5)-VL(2))

<400> 63

```

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1           5           10           15

```

```

Val His Ser Glu Leu Val Met Thr Gln Ser Pro Ser Ser Leu Thr Val
          20           25           30

```

```

Thr Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu
          35           40           45

```

```

Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys
          50           55           60

```

```

Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu
65           70           75           80

```

Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe
85 90 95

Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr
100 105 110

Cys Gln Asn Asp Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys
115 120 125

Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
130 135 140

Gly Gly Ser Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val
145 150 155 160

Arg Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala
165 170 175

Phe Thr Asn Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly
180 185 190

Leu Glu Trp Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr
195 200 205

Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser
210 215 220

Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala
225 230 235 240

Val Tyr Phe Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr
245 250 255

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
260 265 270

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
275 280 285

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
290 295 300

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile

305 310 315 320

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
 325 330 335

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
 340 345 350

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
 355 360 365

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 370 375 380

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
385 390 395 400

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
 405 410 415

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
 420 425 430

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 435 440 445

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 450 455 460

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
465 470 475 480

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 485 490 495

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 500 505 510

Glu Ile Lys
 515

<210> 64
<211> 1500
<212> DNA
<213> artificial sequence

<220>

<223> VH5/VL2x3-5

<400> 64

gacgtccaac	tggtgcagtc	aggggctgaa	gtgaaaaaac	ctggggcctc	agtgaagggtg	60
tcctgcaagg	cttctggcta	cacctttact	aggtacacga	tgactgggt	aaggcaggca	120
cctggacagg	gtctggaatg	gattggatac	attaatccta	gccgtgggta	tactaattac	180
gcagacagcg	tcaagggccg	cttcacaatc	actacagaca	aatccaccag	cacagcctac	240
atggaactga	gcagcctgcg	ttctgaggac	actgcaacct	attactgtgc	aagatattat	300
gatgatcatt	actgccttga	ctactggggc	caaggcacca	cggtcaccgt	ctcctcaggc	360
gaaggtaacta	gtactgggtc	tggtggaagt	ggagggttcag	gtggagcaga	cgacattgta	420
ctgaccagtc	ctccagcaac	tctgtctctg	tctccagggg	agcgtgccac	cctgagctgc	480
agagccagtc	aaagtgtgtaag	ttacatgaac	tggtaccagc	agaagccggg	caaggcaccc	540
aaaagatgga	tttatgacac	atccaaagtg	gcttctggag	tccctgctcg	cttcagtggc	600
agtgggtctg	ggaccgacta	ctctctcaca	atcaacagct	tggaggctga	agatgctgcc	660
acttattact	gccaacagtg	gagtagtaac	ccgctcacgt	tcggtggcgg	gaccaagggtg	720
gagatcaaata	ccggagggtg	tggatccgag	gtgcagctgc	tcgagcagtc	tggagctgag	780
ctggtaaggc	ctgggacttc	agtgaagctg	tcctgcaagg	cttctggcta	caccttcaca	840
agctatgggt	taagctgggt	gaagcagaga	actggacagg	gccttgagtg	gattggagag	900
gtttatccta	gaattggtaa	tgcttactac	aatgagaagt	tcaagggcaa	ggccacactg	960
actgcagaca	aatcctccag	cacagcgtcc	atggagctcc	gcagcctgac	atctgaggac	1020
tctgcggtct	atttctgtgc	aagacgggga	tcctacggta	gtaactacga	ctggtacttc	1080
gatgtctggg	gccaagggac	cacggtcacc	gtctcctcag	gtggtgggtg	ttctggcggc	1140
ggcggctccg	gtggtgggtg	ttctgagctc	gtgatgacc	agactccact	ctccctgcct	1200
gtcagtcttg	gagatcaagc	ctccatctct	tgagatcta	gtcagagcct	tgtacacagt	1260
aatggaaaca	cctattttaca	ttggtacctg	cagaagccag	gccagtctcc	aaagctcctg	1320
atctacaaag	tttccaaccg	attttctggg	gtcccagaca	ggttcagtgg	cagtggatca	1380
gggacagatt	tcacactcaa	gatcagcaga	gtggaggctg	aggatctggg	agtttatttc	1440
tgctctcaaa	gtacacatgt	tccgtacacg	ttcggagggg	ggaccaagct	tgagatcaaa	1500

<210> 65

<211> 500

<212> PRT

<213> artificial sequence

<220>

<223> VH5/VL2x3-5

<400> 65

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln
245 250 255

Ser Gly Ala Glu Leu Val Arg Pro Gly Thr Ser Val Lys Leu Ser Cys
260 265 270

Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Gly Leu Ser Trp Val Lys
275 280 285

Gln Arg Thr Gly Gln Gly Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg
290 295 300

Ile Gly Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu
305 310 315 320

Thr Ala Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu
325 330 335

Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr
340 345 350

Gly Ser Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr
355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
370 375 380

Gly Gly Gly Ser Glu Leu Val Met Thr Gln Thr Pro Leu Ser Leu Pro
385 390 395 400

Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
405 410 415

Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys
420 425 430

Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe
435 440 445

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
450 455 460

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe
465 470 475 480

Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys
485 490 495

Leu Glu Ile Lys
500

<210> 66

<211> 1491

<212> DNA

<213> artificial sequence

<220>

<223> VH5/VL2x4-1

<400> 66

gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaaggtg 60
tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 120
cctggacagg gtctggaatg gattggatac attaataccta gccgtgggta tactaattac 180
gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 240
atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc 360
gaaggtaacta gtactgggtc tgggtggaagt ggagggttcag gtggagcaga cgacattgta 420
ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc 480
agagccagtc aaagtgtgaa ttacatgaac tgggtaccagc agaagccggg caaggcaccc 540
aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcgggtggcg gaccaagggtg 720
gagatcaaata ccggagggtg tggatccgag gtgcagctgc tcgagcagtc tggagctgag 780
ctggtaaggc ctgggacttc agtgaagata tcctgcaagg cttctggata cgccttcact 840
aactactggc taggttgggt taagcagagg cctggacatg gacttgaatg gggtggagat 900
atcttccctg gaagtggtaa tgctcactac aatgagaagt tcaagggcaa agccacactg 960
actgcagaca agtcctcgta cacagcctat atgcagctca gtagcctgac atctgaggac 1020

tctgctgtct atttctgtgc aagattgctg aactgggacg aggctatgga ctactggggc 1080
caagggacca cggtcaccgt ctcttcaggt ggtggtggtt ctggcggcgg cggctccggt 1140
ggtggtggtt ctgagctcgt gatgacacag tctccatcct ccctgagtgt gtcagcagga 1200
gagaagggtca ctatgagctg caagtccagt cagagtctgt taaacagtgg aaatcaaaag 1260
aactacttgg cctggtacca gcagaaacca gggcagcctc ctaaactgtt gatctacggg 1320
gcatccacta ggggaatctgg ggtccctgat cgcttcacag gcagtggatc tggaacagat 1380
ttcactctca ccatcagcag tgtgcaggct gaagacctgg cagtttatta ctgtcagaat 1440
gattatagtt atccgtacac gttcggaggg gggaccaagc ttgagatcaa a 1491

<210> 67
<211> 497
<212> PRT
<213> artificial sequence

<220>
<223> VH5/VL2x4-1

<400> 67

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
 130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
 145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln
 245 250 255

Ser Gly Ala Glu Leu Val Arg Pro Gly Thr Ser Val Lys Ile Ser Cys
 260 265 270

Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Trp Leu Gly Trp Val Lys
 275 280 285

Gln Arg Pro Gly His Gly Leu Glu Trp Val Gly Asp Ile Phe Pro Gly
 290 295 300

Ser Gly Asn Ala His Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu
 305 310 315 320

Thr Ala Asp Lys Ser Ser Tyr Thr Ala Tyr Met Gln Leu Ser Ser Leu
 325 330 335

Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Leu Arg Asn Trp
 340 345 350

Asp Glu Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser
 355 360 365

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 370 375 380

Glu Leu Val Met Thr Gln Ser Pro Ser Ser Leu Ser Val Ser Ala Gly
 385 390 395 400

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
 405 410 415

Gly Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 420 425 430

Pro Pro Lys Leu Leu Ile Tyr Gly Ala Ser Thr Arg Glu Ser Gly Val
 435 440 445

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 450 455 460

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Asn
 465 470 475 480

Asp Tyr Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
 485 490 495

Lys

<210> 68
 <211> 18
 <212> PRT
 <213> artificial sequence

<220>
 <223> non-deimmunized linker sequence

<400> 68

Val Glu Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly
 1 5 10 15

Val Asp

<210> 69
 <211> 357
 <212> DNA

<213> artificial sequence

<220>

<223> anti-CD3 VH2

<400> 69

```

gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaagggtg      60
tcctgcaagg cttctggcta caccgctact aggtacacga tgcactgggt aaggcaggca      120
cctggacagg gtctggaatg gattggatac attaataccta gccgtgggta tactaattac      180
gcacagaagt tgcagggccg cgtcacaatg actacagaca cttccaccag cacagcctac      240
atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat      300
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctca          357

```

<210> 70

<211> 119

<212> PRT

<213> artificial sequence

<220>

<223> anti-CD3 VH2

<400> 70

```

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1           5           10           15

```

```

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ala Thr Arg Tyr
20           25           30

```

```

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35           40           45

```

```

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Gln Lys Leu
50           55           60

```

```

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65           70           75           80

```

```

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
85           90           95

```

```

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100          105          110

```

```

Thr Thr Val Thr Val Ser Ser
115

```

<210> 71
 <211> 357
 <212> DNA
 <213> artificial sequence

<220>
 <223> anti-CD3 VH3

<400> 71
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 tcctgcaagg cttctggcta caccgctact aggtacacga tgcactgggt aaggcaggca 120
 cctggacagg gtctggaatg gattggatac attaataccta gccgtgggtta tactaattac 180
 gcacagaagt tgcagggccg cgtcacaatg actacagaca cttccaccag cacagcctac 240
 ctgcaaataa acagcctgaa aactgaggac actgcagtct attactgtgc aagatattat 300
 gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctcctca 357

<210> 72
 <211> 119
 <212> PRT
 <213> artificial sequence

<220>
 <223> anti-CD3 VH3

<400> 72

Asp	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala	
1				5					10					15		
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Ala	Thr	Arg	Tyr	
			20					25					30			
Thr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile	
		35					40					45				
Gly	Tyr	Ile	Asn	Pro	Ser	Arg	Gly	Tyr	Thr	Asn	Tyr	Ala	Gln	Lys	Leu	
	50					55					60					
Gln	Gly	Arg	Val	Thr	Met	Thr	Thr	Asp	Thr	Ser	Thr	Ser	Thr	Ala	Tyr	
65					70					75					80	
Leu	Gln	Met	Asn	Ser	Leu	Lys	Thr	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
				85					90					95		
Ala	Arg	Tyr	Tyr	Asp	Asp	His	Tyr	Cys	Leu	Asp	Tyr	Trp	Gly	Gln	Gly	

100

105

110

Thr Thr Val Thr Val Ser Ser
115

<210> 73

<211> 357

<212> DNA

<213> artificial sequence

<220>

<223> anti-CD3 VH5

<400> 73

gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaagggtg 60

tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 120

cctggacagg gtctggaatg gattggatac attaatccta gccgtgggta tactaattac 180

gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 240

atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300

gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctcctca 357

<210> 74

<211> 119

<212> PRT

<213> artificial sequence

<220>

<223> anti-CD3 VH5

<400> 74

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

```
<210> 75
<211> 357
<212> DNA
<213> artificial sequence
```

<220>
<223> anti-CD3 VH7

[illegible]

```
<210> 76
<211> 119
<212> PRT
<213> artificial sequence
```

<220>
<223> anti-CD3 VH7

<400> 76

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 77
<211> 318
<212> DNA
<213> artificial sequence

<220>
<223> anti-CD3 VL1

<400> 77
gacattcaga tgaccagtc tccatctagc ctgtctgcat ctgtcgggga ccgtgtcacc 60
atcacctgca gagccagtca aagtgttaagt tacatgaact ggtaccagca gaagccgggc 120
aaggcaccca aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctcgc 180
ttcagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa 240
gatgctgccca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cggtggcggg 300
accaaggtgg agatcaaaa 318

<210> 78
<211> 106
<212> PRT
<213> artificial sequence

<220>
<223> anti-CD3 VL1

<400> 78

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
 85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 79
 <211> 318
 <212> DNA
 <213> artificial sequence

<220>
 <223> anti-CD3 VL2

<400> 79
 gacattgtac tgaccagtc tccagcaact ctgtctctgt ctccagggga gcgtgccacc 60
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 aaggcaccca aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctcgc 180
 ttcagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa 240
 gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cggtggcggg 300
 accaaggtgg agatcaaa 318

<210> 80
 <211> 106
 <212> PRT
 <213> artificial sequence

<220>
 <223> anti-CD3 VL2

<400> 80

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
 20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr

35

40

45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
 85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 81
 <211> 318
 <212> DNA
 <213> artificial sequence

<220>
 <223> anti-CD3 VL3

<400> 81
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 ctgacctgca gagccagttc aagtgttaagt tacatgaact ggtaccagca gaagccgggc 120
 aaggcaccca aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctcgc 180
 ttcagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa 240
 gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cggtggcggg 300
 accaagggtg agatcaaa 318

<210> 82
 <211> 106
 <212> PRT
 <213> artificial sequence

<220>
 <223> anti-CD3 VL3

<400> 82

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met
 20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
 35 40 45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
 85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 83
 <211> 30
 <212> DNA
 <213> artificial sequence

<220>
 <223> vH CDR1 anti-CD3 wt

<400> 83
 ggctacacct ttactaggta cacgatgcac

30

<210> 84
 <211> 10
 <212> PRT
 <213> artificial sequence

<220>
 <223> vH CDR1 anti-CD3 wt

<400> 84

Gly Tyr Thr Phe Thr Arg Tyr Thr Met His
 1 5 10

<210> 85
 <211> 30
 <212> DNA
 <213> artificial sequence

<220>
 <223> vH CDR1 VH2,3

<400> 85
 ggctacaccg ctactaggta cacgatgcac

30

<210> 86

<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> vH CDR1 VH2,3

<400> 86

Gly Tyr Thr Ala Thr Arg Tyr Thr Met His
1 5 10

<210> 87
<211> 30
<212> DNA
<213> artificial sequence

<220>
<223> vH CDR1 VH5,7

<400> 87
ggctacacct ttactaggta cacgatgcac

30

<210> 88
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> vH CDR1 VH5,7

<400> 88

Gly Tyr Thr Phe Thr Arg Tyr Thr Met His
1 5 10

<210> 89
<211> 51
<212> DNA
<213> artificial sequence

<220>
<223> vH CDR2 wt anti-CD3 VH7

<400> 89
tacattaatc ctagccgtgg ttataactaat tacaatcaga agttcaagga c

51

<210> 90
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> vH CDR2 wt anti-CD3 VH7

<400> 90

Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys
1 5 10 15

Asp.

<210> 91

<211> 51

<212> DNA

<213> artificial sequence

<220>

<223> vH CDR2 VH5

<400> 91

tacattaatc ctagccgtgg ttataactaat tacgcagaca gcgtcaaggg c

51

<210> 92

<211> 17

<212> PRT

<213> artificial sequence

<220>

<223> vH CDR2 VH5

<400> 92

Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 93

<211> 51

<212> DNA

<213> artificial sequence

<220>

<223> vH CDR2 VH2,3

<400> 93

tacattaatc ctagccgtgg ttataactaat tacgcacaga agttgcaggg c

51

<210> 94

<211> 17

<212> PRT

<213> artificial sequence

<220>

<223> vH CDR2 VH2,3

<400> 94

Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Gln Lys Leu Gln
1 5 10 15

Gly

<210> 95

<211> 30

<212> DNA

<213> artificial sequence

<220>

<223> vH CDR3 wt anti-CD3 VH2,3,5,7

<400> 95

tattatgatg atcattactg ccttgactac

30

<210> 96

<211> 10

<212> PRT

<213> artificial sequence

<220>

<223> vH CDR3 wt anti-CD3 VH2,3,5,7

<400> 96

Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr
1 5 10

<210> 97

<211> 30

<212> DNA

<213> artificial sequence

<220>

<223> vK CDR1 wt anti-CD3 VL3

<400> 97

agagccagtt caagtgtgtaag ttacatgaac

30

<210> 98

<211> 10

<212> PRT

<213> artificial sequence

<220>

<223> vK CDR1 wt anti-CD3 VL3

<400> 98

Arg Ala Ser Ser Ser Val Ser Tyr Met Asn
1 5 10

<210> 99
<211> 30
<212> DNA
<213> artificial sequence

<220>
<223> vK CDR1 VL 1,2

<400> 99
agagccagtc aaagtgtaag ttacatgaac

30

<210> 100
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> vK CDR1 VL 1,2

<400> 100

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn
1 5 10

<210> 101
<211> 21
<212> DNA
<213> artificial sequence

<220>
<223> vK CDR2 wt anti-CD3 VL1-3

<400> 101
gacacatcca aagtggcttc t

21

<210> 102
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> vK CDR2 wt anti-CD3 VL1-3

<400> 102

Asp Thr Ser Lys Val Ala Ser
1 5

<210> 103
<211> 27
<212> DNA

<213> artificial sequence

<220>

<223> vK CDR3 wt anti-CD3 VL1-3

<400> 103

caacagtgga gtagtaaccc gctcacg

27

<210> 104

<211> 9

<212> PRT

<213> artificial sequence

<220>

<223> vK CDR3 wt anti-CD3 VL1-3

<400> 104

Gln Gln Trp Ser Ser Asn Pro Leu Thr

1

5

<210> 105

<211> 357

<212> DNA

<213> artificial sequence

<220>

<223> vH anti-CD3 with the mutations of cys->ser

<400> 105

gatatcaaac tgcagcagtc aggggctgaa ctggcaagac ctggggcctc agtgaagatg 60

tcctgcaaga cttctggcta cacctttact aggtacacga tgcactgggt aaaacagagg 120

cctggacagg gtctggaatg gattggatac attaatccta gccgtgggta tactaattac 180

aatcagaagt tcaaggacaa ggccacattg actacagaca aatcctccag cacagcctac 240

atgcaactga gcagcctgac atctgaggac tctgcagtct attactgtgc aagatattat 300

gatgatcatt actcccttga ctactggggc caaggcacca ctctcacagt ctctctca 357

<210> 106

<211> 119

<212> PRT

<213> artificial sequence

<220>

<223> vH anti-CD3 with the mutations of cys ->ser

<400> 106

Asp Ile Lys Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala

1

5

10

15

Ser Val Lys Met Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30

Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
 50 55 60

Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Ser Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Leu Thr Val Ser Ser
 115

<210> 107

<211> 30

<212> DNA

<213> artificial sequence

<220>

<223> vH CDR3 anti-CD3 with the mutation cys-> ser

<400> 107

tattatgatg atcattactc ccttgactac

30

<210> 108

<211> 10

<212> PRT

<213> artificial sequence

<220>

<223> vH CDR3 anti-CD3 with the mutation cys-> ser

<400> 108

Tyr Tyr Asp Asp His Tyr Ser Leu Asp Tyr
 1 5 10

<210> 109

<211> 357

<212> DNA

<213> artificial sequence

<220>

<223> wild type anti-CD3 VH

<400> 109

gatatcaaac tgcagcagtc aggggctgaa ctggcaagac ctggggcctc agtgaagatg 60

tcctgcaaga cttctggcta cacctttact aggtacacga tgcactgggt aaaacagagg 120

cctggacagg gtctggaatg gattggatac attaatccta gccgtgggtta tactaattac 180

aatcagaagt tcaaggacaa ggccacattg actacagaca aatcctccag cacagcctac 240

atgcaactga gcagcctgac atctgaggac tctgcagtct attactgtgc aagatattat 300

gatgatcatt actgccttga ctactggggc caaggcacca ctctcacagt ctctca 357

<210> 110

<211> 119

<212> PRT

<213> artificial sequence

<220>

<223> wild type anti-CD3 VH

<400> 110

Asp	Ile	Lys	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Ala	Arg	Pro	Gly	Ala
1			5						10					15	

Ser	Val	Lys	Met	Ser	Cys	Lys	Thr	Ser	Gly	Tyr	Thr	Phe	Thr	Arg	Tyr
			20					25					30		

Thr	Met	His	Trp	Val	Lys	Gln	Arg	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile
		35					40					45			

Gly	Tyr	Ile	Asn	Pro	Ser	Arg	Gly	Tyr	Thr	Asn	Tyr	Asn	Gln	Lys	Phe
	50					55					60				

Lys	Asp	Lys	Ala	Thr	Leu	Thr	Thr	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr
65					70					75					80

Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys
				85					90					95	

Ala	Arg	Tyr	Tyr	Asp	Asp	His	Tyr	Cys	Leu	Asp	Tyr	Trp	Gly	Gln	Gly
			100					105					110		

Thr	Thr	Leu	Thr	Val	Ser	Ser
						115

<210> 111
 <211> 318
 <212> DNA
 <213> artificial sequence

<220>
 <223> wild type anti-CD3 VK

<400> 111
 gacattcagc tgaccagtc tccagcaatc atgtctgcat ctccagggga gaaggtcacc 60
 atgacctgca gagccagttc aagtgttaagt tacatgaact ggtaccagca gaagtcaggc 120
 acctccccca aaagatggat ttatgacaca tccaaagtgg cttctggagt cccttatcgc 180
 ttcagtggca gtgggtctgg gacctcatatc tctctcacia tcagcagcat ggaggctgaa 240
 gatgctgccca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cggtgctggg 300
 accaagctgg agctgaaa 318

<210> 112
 <211> 106
 <212> PRT
 <213> artificial sequence

<220>
 <223> wild type anti-CD3 VK

<400> 112

Asp Ile Gln Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
 1 5 10 15

Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met
 20 25 30

Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
 35 40 45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Tyr Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
 85 90 95

Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 100 105

<210> 113
 <211> 372
 <212> DNA
 <213> artificial sequence

<220>
 <223> CD19 VH

<400> 113
 caggtgcagc tgcagcagtc tggggctgag ctggtgaggc ctgggtcctc agtgaagatt 60
 tcctgcaagg cttctggcta tgcattcagt agctactgga tgaactgggt gaagcagagg 120
 cctggacagg gtcttgagtg gattggacag atttggcctg gagatgggtga tactaactac 180
 aatggaaagt tcaagggtaa agccactctg actgcagacg aatcctccag cacagcctac 240
 atgcaactca gcagcctagc atctgaggac tctgcggtct atttctgtgc aagacgggag 300
 actacgacgg taggccgtta ttactatgct atggactact ggggcccaagg gaccacggtc 360
 accgtctcct cc 372

<210> 114
 <211> 124
 <212> PRT
 <213> artificial sequence

<220>
 <223> CD19 VH

<400> 114
 Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser
 1 5 10 15
 Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr
 20 25 30
 Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe
 50 55 60
 Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr
 65 70 75 80
 Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys
 85 90 95

Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp
 100 105 110

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 115
 <211> 333
 <212> DNA
 <213> artificial sequence

<220>
 <223> CD19 VL

<400> 115
 gatatccagc tgaccagtc tccagcttct ttggctgtgt ctctagggca gagggccacc 60
 atctcctgca aggccagcca aagtgttgat tatgatgggtg atagttattt gaactgggtac 120
 caacagattc caggacagcc acccaaactc ctcatctatg atgcatccaa tctagtttct 180
 gggatcccac ccaggtttag tggcagtggg tctgggacag acttcaccct caacatccat 240
 cctgtggaga aggtggatgc tgcaacctat cactgtcagc aaagtactga ggatccgtgg 300
 acgttcggtg gagggaccaa gctcgagatc aaa 333

<210> 116
 <211> 111
 <212> PRT
 <213> artificial sequence

<220>
 <223> CD19 VL

<400> 116

Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
 20 25 30

Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
 35 40 45

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
 65 70 75 80

Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
85 90 95

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 117
<211> 47
<212> DNA
<213> artificial sequence

<220>
<223> 4-7 VL BspEI FOR

<400> 117
ctgaaatccg gaggtggtgg atccgagctc gtgatgaccc agactcc 47

<210> 118
<211> 52
<212> DNA
<213> artificial sequence

<220>
<223> 4-7 VL GS15 REV

<400> 118
ggagccgccg ccgccagaac caccaccacc tttgatctca agcttggtcc cc 52

<210> 119
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDRH3 M1 mutant

<400> 119

His Tyr Asp Asp His Tyr Cys Leu Asp Tyr
1 5 10

<210> 120
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDRH3 M4 mutant

<400> 120

Tyr Ser Asp Asp His Tyr Cys Leu Asp Tyr
1 5 10

<210> 121
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDRH3 M7 mutant

<400> 121

Tyr Tyr Asp Ala His Tyr Cys Leu Asp Tyr
1 5 10

<210> 122
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDRH3 M9 mutant

<400> 122

Tyr Tyr Asp Asp Gln Tyr Cys Leu Asp Tyr
1 5 10

<210> 123
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDRH3 M10 mutant

<400> 123

Tyr Tyr Asp Asp Pro Tyr Cys Leu Asp Tyr
1 5 10

<210> 124
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDRH3 M11 mutant

<400> 124

Tyr Phe Asn Asp His Tyr Cys Leu Asp Tyr
1 5 10

<210> 125

<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDRH3 M13 mutant

<400> 125

Tyr Tyr Asn Asp Gln Tyr Cys Leu Asp Tyr
1 5 10

<210> 126
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDRH3 M20 mutant

<400> 126

Tyr His Asp Asp Pro Tyr Cys Leu Asp Tyr
1 5 10

<210> 127
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDRH3 M76 mutant

<400> 127

Tyr Tyr Asp Asp Asn Tyr Cys Leu Asp Tyr
1 5 10

<210> 128
<211> 354
<212> DNA
<213> artificial sequence

<220>
<223> CCR5 Heavy chain

<400> 128

cagctggagc agtctggacc tgaactgaag aagcctggag agacagtcac gatctcctgc 60
aaggcttctg ggtatacctt cacgaagttc ggaatgaact gggatgaagca ggctccagga 120
aagggtttta agtggatggg ctggatacac acctccactg gagagccaac atattctgat 180
gacttcaagg gacggtttgc cttctctttg gaaacgtctg ccagcactgc ctatttgcg 240
atcaacaacc tcaaaaatga ggacatggct aaatacttct gtgccagagg tggtccttac 300

gtaaggggtg ctttggacta ctgggggtcaa ggaacctcag tcaccgtctc ctcc 354

<210> 129
 <211> 118
 <212> PRT
 <213> artificial sequence

<220>
 <223> CCR5 Heavy chain

<400> 129

Gln Leu Glu Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu Thr Val
 1 5 10 15

Thr Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Lys Phe Gly Met
 20 25 30

Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met Gly Trp
 35 40 45

Ile His Thr Ser Thr Gly Glu Pro Thr Tyr Ser Asp Asp Phe Lys Gly
 50 55 60

Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr Leu Arg
 65 70 75 80

Ile Asn Asn Leu Lys Asn Glu Asp Met Ala Lys Tyr Phe Cys Ala Arg
 85 90 95

Gly Gly Pro Tyr Val Arg Gly Ala Leu Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Ser Val Thr Val Ser Ser
 115

<210> 130
 <211> 333
 <212> DNA
 <213> artificial sequence

<220>
 <223> CCR5 Light chain

<400> 130

gacattatcc tgatccaatc tccaccttct ttggctgtgt ctctagggca gagggccacc 60

atctcctgca gaaccagcga aaatgttgac ggatacggca ttagttttat aaactggtac 120

caacagaagc caggacagcc acccaaactc ctcatctatg ctgcatccca ccaaggatcc 180
 ggggtccctg ccagatttag tggcagtggg tctgggacag acttcagcct caacatccat 240
 cctttggagg aggatgatac tgcaatgtat ttctgtcacc aaagtaagaa ggttccgtgg 300
 acgttcggtg gaggcaccaa gctggaaatc aaa 333

<210> 131
 <211> 111
 <212> PRT
 <213> artificial sequence

<220>
 <223> CCR5 Light chain

<400> 131

Asp Ile Ile Leu Ile Gln Ser Pro Pro Ser Leu Ala Val Ser Leu Gly
 1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Arg Thr Ser Glu Asn Val Asp Gly Tyr
 20 25 30

Gly Ile Ser Phe Ile Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45

Lys Leu Leu Ile Tyr Ala Ala Ser His Gln Gly Ser Gly Val Pro Ala
 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Asn Ile His
 65 70 75 80

Pro Leu Glu Glu Asp Asp Thr Ala Met Tyr Phe Cys His Gln Ser Lys
 85 90 95

Lys Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105 110

<210> 132
 <211> 360
 <212> DNA
 <213> artificial sequence

<220>
 <223> EpCAM5-10 heavy chain

<400> 132

gaggtgcagc tgctcgagca gtctggagct gagctggtaa ggcctgggac ttcagtgaag 60
 atatcctgca aggcttctgg atacgccttc actaactact ggctagggttg ggtaaagcag 120

aggcctggac atggacttga gtggattgga gatattttcc ctggaagtgg taatatccac 180
tacaatgaga agttcaaggg caaagccaca ctgactgcag acaaattcttc gagcacagcc 240
tatatgcagc tcagtagcct gacatttgag gactctgctg tctattttctg tgcaagactg 300
aggaactggg acgagcctat ggactactgg ggccaaggga ccacgggtcac cgtctcctca 360

<210> 133
<211> 120
<212> PRT
<213> artificial sequence

<220>
<223> EpCAM5-10 heavy chain

<400> 133

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
1 5 10 15

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
20 25 30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
35 40 45

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
65 70 75 80

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
85 90 95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 134
<211> 339
<212> DNA
<213> artificial sequence

<220>
<223> EpCAM5-10 light chain

<400> 134
gagctcgtga tgacacagtc tccatcctcc ctgactgtga cagcaggaga gaaggtcact 60
atgagctgca agtccagtcga gagtctgtta aacagtggaa atcaaaagaa ctacttgacc 120
tgggtaccagc agaaaccagg gcagcctcct aaactgttga tctactgggc atccactagg 180
gaatctgggg tccctgatcg cttcacaggc agtggatctg gaacagattt cactctcacc 240
atcagcagtg tgcaggctga agacctggca gtttattact gtcagaatga ttatagttat 300
ccgctcacgt tcggtgctgg gaccaagctt gagatcaaa 339

<210> 135
<211> 113
<212> PRT
<213> artificial sequence
<220>
<223> EpCAM 5-10 light chain

<400> 135

Glu Leu Val Met Thr Gln Ser Pro Ser Ser Leu Thr Val Thr Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Asp Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile
100 105 110

Lys

<210> 136
<211> 360

<212> DNA

<213> artificial sequence

<220>

<223> EpCAM 3-1 VH

<400> 136

gaggtgcagc tgctcgagca gtctggagct gagctgggtga aacctggggc ctcaagtgaag 60
atatacctgca aggcttctgg atacgccttc actaactact ggctagggttg ggtaaagcag 120
aggcctggac atggacttga gtggattgga gatcttttcc ctggaagtgg taatactcac 180
tacaatgaga ggttcagggg caaagccaca ctgactgcag acaaatcctc gagcacagcc 240
tttatgcagc tcagtagcct gacatctgag gactctgctg tctatttctg tgcaagattg 300
aggaactggg acgaggctat ggactactgg ggccaaggga ccacggtcac cgtctcctca 360

<210> 137

<211> 120

<212> PRT

<213> artificial sequence

<220>

<223> EpCAM 3-1 VH

<400> 137

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Lys Pro Gly
1 5 10 15

Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
20 25 30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
35 40 45

Ile Gly Asp Leu Phe Pro Gly Ser Gly Asn Thr His Tyr Asn Glu Arg
50 55 60

Phe Arg Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
65 70 75 80

Phe Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe
85 90 95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser

115

120

<210> 138
 <211> 321
 <212> DNA
 <213> artificial sequence

<220>
 <223> EpCAM 3-1 VL

<400> 138
 gagctcgtca tgaccagtc tccatcttat cttgctgcat ctctggaga aaccattact 60
 attaattgca gggcaagtaa gagcattagc aaatatttag cctgggtatca agagaaacct 120
 gggaaaacta ataagcttct tatctactct ggatccactt tgcaatctgg aattccatca 180
 aggttcagtg gcagtggatc tggtagatc ttcactctca ccatcagtag cctggagcct 240
 gaagattttg caatgtatta ctgtcaacag cataatgaat atccgtacac gttcggaggg 300
 gggaccaagc ttgagatcaa a 321

<210> 139
 <211> 107
 <212> PRT
 <213> artificial sequence

<220>
 <223> EpCAM 3-1 VL

<400> 139

Glu Leu Val Met Thr Gln Ser Pro Ser Tyr Leu Ala Ala Ser Pro Gly
 1 5 10 15

Glu Thr Ile Thr Ile Asn Cys Arg Ala Ser Lys Ser Ile Ser Lys Tyr
 20 25 30

Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Thr Asn Lys Leu Leu Ile
 35 40 45

Tyr Ser Gly Ser Thr Leu Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
 65 70 75 80

Glu Asp Phe Ala Met Tyr Tyr Cys Gln Gln His Asn Glu Tyr Pro Tyr
 85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 140
 <211> 372
 <212> DNA
 <213> artificial sequence

<220>
 <223> EpCAM 3-5 VH

<400> 140
 gaggtgcagc tgctcgagca gtctggagct gagctggtaa ggcttgggac ttcagtgaag 60
 ctgtcctgca aggcttctgg ctacaccttc acaagctatg gtttaagctg ggtgaagcag 120
 agaactggac agggccttga gtggattgga gaggtttatc ctagaattgg taatgcttac 180
 tacaatgaga agttcaaggg caaggccaca ctgactgcag acaaatcctc cagcacagcg 240
 tccatggagc tccgcagcct gacatctgag gactctgcgg tctatttctg tgcaagacgg 300
 ggatcctacg gtagtaacta cgactggtag ttcgatgtct ggggccaagg gaccacggtc 360
 accgtctcct ca 372

<210> 141
 <211> 124
 <212> PRT
 <213> artificial sequence

<220>
 <223> EpCAM 3-5 VH

<400> 141

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
 1 5 10 15

Thr Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser
 20 25 30

Tyr Gly Leu Ser Trp Val Lys Gln Arg Thr Gly Gln Gly Leu Glu Trp
 35 40 45

Ile Gly Glu Val Tyr Pro Arg Ile Gly Asn Ala Tyr Tyr Asn Glu Lys
 50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
 65 70 75 80

Ser Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe

85

90

95

Cys Ala Arg Arg Gly Ser Tyr Gly Ser Asn Tyr Asp Trp Tyr Phe Asp
 100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 142
 <211> 336
 <212> DNA
 <213> artificial sequence

<220>
 <223> EpCAM 3-5 VL

<400> 142
 gagctcgtga tgaccagac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc 60
 atctcttgca gatctagtca gaggcttgta cacagtaatg gaaacaccta ttacattgg 120
 tacctgcaga agccaggcca gtctccaaag ctctgatct acaaagtttc caaccgattt 180
 tctgggggtcc cagacagggt cagtggcagt ggatcaggga cagatttcac actcaagatc 240
 agcagagtgg aggctgagga tctgggagtt tatttctgct ctcaaagtac acatgttccg 300
 tacacgttcg gaggggggac caagcttgag atcaaa 336

<210> 143
 <211> 112
 <212> PRT
 <213> artificial sequence

<220>
 <223> EpCAM 3-5 VL

<400> 143

Glu Leu Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
 1 5 10 15

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
 20 25 30

Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
 50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser
85 90 95

Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 144
<211> 360
<212> DNA
<213> artificial sequence

<220>
<223> EpCAM 4-1 VH

<400> 144
gaggtgcagc tgctcgagca gtctggagct gagctggtaa ggcctgggac ttcagtgaag 60
atatcctgca aggcttctgg atacgccttc actaactact ggctagggttg ggttaagcag 120
aggcctggac atggacttga atggggttga gatattttcc ctggaagtgg taatgctcac 180
tacaatgaga agttcaaggg caaagccaca ctgactgcag acaagtcctc gtacacagcc 240
tatatgcagc tcagtagcct gacatctgag gactctgctg tctatttctg tgcaagattg 300
cggaactggg acgaggctat ggactactgg ggccaaggga ccacggtcac cgtctcctca 360

<210> 145
<211> 120
<212> PRT
<213> artificial sequence

<220>
<223> EpCAM 4-1 VH

<400> 145

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
1 5 10 15

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
20 25 30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
35 40 45

Val Gly Asp Ile Phe Pro Gly Ser Gly Asn Ala His Tyr Asn Glu Lys
50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Tyr Thr Ala
65 70 75 80

Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe
85 90 95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 146
<211> 339
<212> DNA
<213> artificial sequence

<220>
<223> EpCAM 4-1 VL

<400> 146
gagctcgtga tgacacagtc tccatcctcc ctgagtgtgt cagcaggaga gaaggcact 60
atgagctgca agtccagtca gagtctgtta aacagtggaa atcaaaagaa ctacttggcc 120
tggtaccagc agaaaccagg gcagcctcct aaactgttga tctacggggc atccactagg 180
gaatctgggg tccctgatcg cttcacaggc agtggatctg gaacagattt cactctcacc 240
atcagcagtg tgcaggctga agacctggca gtttattact gtcagaatga ttatagttat 300
ccgtacacgt tcggaggggg gaccaagctt gagatcaaa 339

<210> 147
<211> 113
<212> PRT
<213> artificial sequence

<220>
<223> EpCAM 4-1 VL

<400> 147

Glu Leu Val Met Thr Gln Ser Pro Ser Ser Leu Ser Val Ser Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Gly Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Gly Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Asp Tyr Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
100 105 110

Lys

<210> 148
<211> 372
<212> DNA
<213> artificial sequence

<220>
<223> EpCAM 4-7 VH

<400> 148
gaggtgcagc tgctcgagca gtctggagct gagctggcga ggcctggggc ttcagtgaag 60
ctgtcctgca aggcttctgg ctacaccttc acaaactatg gtttaagctg ggtgaagcag 120
aggcctggac aggtccttga gtggattgga gaggtttatc ctagaattgg taatgcttac 180
tacaatgaga agttcaaggg caaggccaca ctgactgcag acaaatcctc cagcacagcg 240
tccatggagc tccgcagcct gacctctgag gactctgcgg tctatttctg tgcaagacgg 300
ggatcctacg atactaacta cgactggtac ttcgatgtct ggggccaagg gaccacggtc 360
accgtctcct ca 372

<210> 149
<211> 124
<212> PRT
<213> artificial sequence

<220>
<223> EpCAM 4-7 VH

<400> 149

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly
1 5 10 15

Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn
20 25 30

Tyr Gly Leu Ser Trp Val Lys Gln Arg Pro Gly Gln Val Leu Glu Trp
35 40 45

Ile Gly Glu Val Tyr Pro Arg Ile Gly Asn Ala Tyr Tyr Asn Glu Lys
50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
65 70 75 80

Ser Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe
85 90 95

Cys Ala Arg Arg Gly Ser Tyr Asp Thr Asn Tyr Asp Trp Tyr Phe Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 150
<211> 336
<212> DNA
<213> artificial sequence

<220>
<223> EpCAM 4-7 VL

<400> 150
gagctcgtga tgacccagac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc 60
atctcttgca gatctagtca gagccttgta cacagtaatg gaaacaccta ttacattgg 120
tacctgcaga agccaggcca gtctccaaag ctctgatct acaaagtttc caaccgattt 180
tctgggggtcc cagacaggtt cagtggcagt ggatcaggga cagatttcac actcaagatc 240
agcagagtgg aggctgagga tctgggagtt tatttctgct ctcaaagtac acatgttccg 300
tacacgttcg gaggggggac caagcttgag atcaaa 336

<210> 151
<211> 112
<212> PRT
<213> artificial sequence

<220>
<223> EpCAM 4-7 VL

<400> 151

Glu Leu Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
1 5 10 15

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser
85 90 95

Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 152

<211> 25

<212> PRT

<213> artificial sequence

<220>

<223> VH5 Framework 1

<400> 152

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser
20 25

<210> 153

<211> 25

<212> PRT

<213> artificial sequence

<220>

<223> VH7 Framework 1

<400> 153

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala

1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser
20 25

<210> 154
<211> 25
<212> PRT
<213> artificial sequence

<220>
<223> VH2 Framework 1

<400> 154

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser
20 25

<210> 155
<211> 25
<212> PRT
<213> artificial sequence

<220>
<223> VH3 Framework 1

<400> 155

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser
20 25

<210> 156
<211> 15
<212> PRT
<213> artificial sequence

<220>
<223> VH5 Framework 2

<400> 156

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr
1 5 10 15

<210> 157
<211> 15

<212> PRT
<213> artificial sequence

<220>
<223> VH7 Framework 2

<400> 157

Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile	Gly	Tyr
1				5					10					15

<210> 158
<211> 22
<212> PRT
<213> artificial sequence

<220>
<223> VH2 Framework 2

<400> 158

Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile	Gly	Tyr	Ile
1				5					10					15	

Asn	Pro	Ser	Arg	Gly	Tyr
				20	

<210> 159
<211> 22
<212> PRT
<213> artificial sequence

<220>
<223> VH3 Framework 2

<400> 159

Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile	Gly	Tyr	Ile
1				5					10					15	

Asn	Pro	Ser	Arg	Gly	Tyr
				20	

<210> 160
<211> 32
<212> PRT
<213> artificial sequence

<220>
<223> VH5 Framework 3

<400> 160

Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu

1 5 10 15

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg
20 25 30

<210> 161
<211> 32
<212> PRT
<213> artificial sequence

<220>
<223> VH7 Framework 3

<400> 161

Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu
1 5 10 15

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 162
<211> 32
<212> PRT
<213> artificial sequence

<220>
<223> VH2 Framework 3

<400> 162

Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr Met Glu
1 5 10 15

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg
20 25 30

<210> 163
<211> 32
<212> PRT
<213> artificial sequence

<220>
<223> VH3 Framework 3

<400> 163

Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 164
<211> 11
<212> PRT
<213> artificial sequence

<220>
<223> VH5 Framework 4

<400> 164

Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser
1				5					10	

<210> 165
<211> 11
<212> PRT
<213> artificial sequence

<220>
<223> VH7 Framework 4

<400> 165

Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser
1				5					10	

<210> 166
<211> 11
<212> PRT
<213> artificial sequence

<220>
<223> VH2 Framework 4

<400> 166

Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser
1				5					10	

<210> 167
<211> 11
<212> PRT
<213> artificial sequence

<220>
<223> VH3 Framework 4

<400> 167

Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser
1				5					10	

<210> 168

<211> 15
<212> PRT
<213> artificial sequence

<220>
<223> Standard linker

<400> 168

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 169
<211> 366
<212> DNA
<213> artificial sequence

<220>
<223> CD20VH

<400> 169

cagggtgcaac tgcggcagcc tggggctgag ctggtgaagc ctggggcctc agtgaagatg 60
tcctgcaagg cttctggcta cacatttacc agttacaata tgcactgggt aaagcagaca 120
cctggacagg gcctggaatg gattggagct atttatccag gaaatgggtga tacttcctac 180
aatcagaagt tcaaaggcaa ggccacattg actgcagaca aatcctccag cacagcctac 240
atgcagctca gcagtctgac atctgaggac tctgcggtct attactgtgc aagatcgcac 300
tacggtagta actacgtaga ctactttgac tactggggcc aaggcacact agtcacagtc 360
tcgaca 366

<210> 170
<211> 122
<212> PRT
<213> artificial sequence

<220>
<223> CD20VH

<400> 170

Gln Val Gln Leu Arg Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Asn Met His Trp Val Lys Gln Thr Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Ser His Tyr Gly Ser Asn Tyr Val Asp Tyr Phe Asp Tyr Trp
 100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Thr
 115 120

<210> 171
 <211> 318
 <212> DNA
 <213> artificial sequence

<220>
 <223> CD20VL

<400> 171
 caaattgttc tctcccagtc tccagcaatc ctttctgcat ctccagggga gaaggtcaca 60
 atgacttgca gggccagctc aagtttaagt ttcatgcact ggtaccagca gaagccagga 120
 tcttccccca aaccctggat ttatgccaca tccaacctgg cttctggagt ccctgctcgc 180
 ttcagtggca gtgggtctgg gacctcttac tctctcacia tcagcagagt ggaggctgaa 240
 gatgctgccca cttatttctg ccatcagtgg agtagtaacc cgctcacgtt cggtgctggg 300
 acaaaggtgg aaataaaa 318

<210> 172
 <211> 106
 <212> PRT
 <213> artificial sequence

<220>
 <223> CD20VL

<400> 172

Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly
 1 5 10 15

Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Leu Ser Phe Met
 20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
35 40 45

Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Phe Cys His Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

Phe Gly Ala Gly Thr Lys Val Glu Ile Lys
100 105

<210> 173
<211> 15
<212> DNA
<213> artificial sequence

<220>
<223> GGGGS linker

<400> 173
ggaggtggtg gatcc

15

<210> 174
<211> 5
<212> PRT
<213> artificial sequence

<220>
<223> GGGGS linker

<400> 174

Gly Gly Gly Gly Ser
1 5

<210> 175
<211> 18
<212> DNA
<213> artificial sequence

<220>
<223> SGGGS linker

<400> 175
tccggaggtg gtggatcc

18

<210> 176
 <211> 6
 <212> PRT
 <213> artificial sequence

<220>
 <223> SGGGS linker

<400> 176

Ser Gly Gly Gly Gly Ser
 1 5

<210> 177
 <211> 1527
 <212> DNA
 <213> artificial sequence

<220>
 <223> antiCD19xantiCD3 VH2VL1

<400> 177

gatatccagc tgaccagtc tccagcttct ttggctgtgt ctctagggca gagggccacc	60
atctcctgca aggccagcca aagtgttgat tatgatgggtg atagttattt gaactgggtac	120
caacagattc caggacagcc acccaaactc ctcatctatg atgcatccaa tctagtttct	180
gggatccac ccaggtttag tggcagtggg tctgggacag acttcaccct caacatccat	240
cctgtggaga aggtggatgc tgcaacctat cactgtcagc aaagtactga ggatccgtgg	300
acgttcggtg gagggaccaa gctcgagatc aaagggtggtg gtggttcttg cggcggcggc	360
tccggtggtg gtggttctca ggtgcagctg cagcagtctg gggctgagct ggtgaggcct	420
gggtcctcag tgaagatttc ctgcaaggct tctggctatg cattcagtag ctactggatg	480
aactgggtga agcagaggcc tggacagggt cttgagtgga ttggacagat ttggcctgga	540
gatggtgata ctaactacaa tggaaagtgc aagggtaaag ccactctgac tgcagacgaa	600
tcctccagca cagcctacat gcaactcagc agcctagcat ctgaggactc tgcggtctat	660
ttctgtgcaa gacgggagac tacgacggta ggccgttatt actatgctat ggactactgg	720
ggccaaggga ccacggtcac cgtctcctcc ggagggtggtg gctccgacgt ccaactggtg	780
cagtcagggg ctgaagtga aaaacctggg gcctcagtga aggtgtcctg caaggcttct	840
ggctacaccg ctactaggta cacgatgcac tgggtaaggc aggcacctgg acagggtctg	900
gaatggattg gatacatata tcctagccgt gggtatacta attacgcaca gaagttgcag	960
ggccgcgtca caatgactac agacacttcc accagcacag cctacatgga actgagcagc	1020
ctgcgttctg aggacactgc aacctattac tgtgcaagat attatgatga tcattactgc	1080

cttgactact ggggccaagg caccacggtc accgtctcct caggcgaagg tactagtact 1140
ggttctgggtg gaagtggagg ttcaggtgga gcagacgaca ttcagatgac ccagtctcca 1200
tctagcctgt ctgcatctgt cggggaccgt gtcacccatca cctgcagagc cagtcaaagt 1260
gtaagttaca tgaactggta ccagcagaag ccgggcaagg cacccaaaag atggatttat 1320
gacacatcca aagtggcttc tggagtcctt gctcgcttca gtggcagtggt gtctgggacc 1380
gactactctc tcacaatcaa cagcttggag gctgaagatg ctgccactta ttactgcca 1440
cagtggagta gtaacccgct cacgttcggt ggcgggacca aggtggagat caaacatcat 1500
caccatcatc attagagatc tgtcgac 1527

<210> 178
<211> 498
<212> PRT
<213> artificial sequence

<220>
<223> antiCD19xantiCD3 VH2VL1

<400> 178

Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
20 25 30

Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65 70 75 80

Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
85 90 95

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
115 120 125

Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val
130 135 140

Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met
145 150 155 160

Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln
165 170 175

Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly
180 185 190

Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln
195 200 205

Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg
210 215 220

Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp
225 230 235 240

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp
245 250 255

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser
260 265 270

Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ala Thr Arg Tyr Thr
275 280 285

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly
290 295 300

Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Gln Lys Leu Gln
305 310 315 320

Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr Met
325 330 335

Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala
340 345 350

Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr
355 360 365

Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly
370 375 380

Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser Pro
385 390 395 400

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
405 410 415

Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
420 425 430

Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly
435 440 445

Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu
450 455 460

Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
465 470 475 480

Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
485 490 495

Ile Lys

<210> 179
<211> 1527
<212> DNA
<213> artificial sequence

<220>
<223> antiCD19xantiCD3 VH2VL2

<400> 179
gatatccagc tgaccagtc tccagcttct ttggctgtgt ctctagggca gagggccacc 60
atctcctgca aggccagcca aagtgttgat tatgatggtg atagttattt gaactggtac 120
caacagattc caggacagcc acccaaactc ctcatctatg atgcatccaa tctagtttct 180
gggatcccac ccaggtttag tggcagtggg tctgggacag acttcaccct caacatccat 240
cctgtggaga aggtggatgc tgcaacctat cactgtcagc aaagtactga ggatccgtgg 300
acgttcggtg gagggaccaa gctcgagatc aaaggtggtg gtggttctgg cggcggcggc 360
tccggtggtg gtggttctca ggtgcagctg cagcagtctg gggctgagct ggtgaggcct 420

gggtcctcag tgaagatttc ctgcaaggct tctggctatg cattcagtag ctactggatg 480
aactgggtga agcagaggcc tggacagggt cttgagtgga ttggacagat ttggcctgga 540
gatggtgata ctaactacaa tggaaagttc aagggtaaag ccactctgac tgcagacgaa 600
tcctccagca cagcctacat gcaactcagc agcctagcat ctgaggactc tgcggtctat 660
ttctgtgcaa gacgggagac tacgacggta ggccgttatt actatgctat ggactactgg 720
ggccaaggga ccacggtcac cgtctcctcc ggagggtggtg gctccgacgt ccaactggtg 780
cagtcagggg ctgaagtga aaaacctggg gcctcagtga aggtgtcctg caaggcttct 840
ggctacaccg ctactaggta cacgatgcac tgggtaaggc aggcacctgg acagggtctg 900
gaatggattg gatacatcaa tcctagccgt gggtatacta attacgcaca gaagttgcag 960
ggccgcgtca caatgactac agacacttcc accagcacag cctacatgga actgagcagc 1020
ctgcgttctg aggacactgc aacctattac tgtgcaagat attatgatga tcattactgc 1080
cttgactact ggggccaagg caccacggtc accgtctcct caggcgaagg tactagtact 1140
ggttctggtg gaagtggagg ttcaggtgga gcagacgaca ttgtactgac ccagtctcca 1200
gcaactctgt ctctgtctcc aggggagcgt gccaccctga gctgcagagc cagtcaaagt 1260
gtaagttaca tgaactggta ccagcagaag ccgggcaagg cacccaaaag atggatttat 1320
gacacatcca aagtggcttc tggagtcctt gctcgcttca gtggcagtgg gtctgggacc 1380
gactactctc tcacaatcaa cagcttggag gctgaagatg ctgccactta ttactgcca 1440
cagtggagta gtaacccgct cacgttcggt ggccgggacca aggtggagat caaacatcat 1500
caccatcatc attagagatc tgtcgac 1527

<210> 180

<211> 498

<212> PRT

<213> artificial sequence

<220>

<223> antiCD19xantiCD3 VH2VL2

<400> 180

Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
20 25 30

Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro

35

40

45

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
 65 70 75 80

Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
 85 90 95

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
 100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
 115 120 125

Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val
 130 135 140

Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met
 145 150 155 160

Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln
 165 170 175

Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly
 180 185 190

Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln
 195 200 205

Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg
 210 215 220

Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp
 225 230 235 240

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp
 245 250 255

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser
 260 265 270

Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ala Thr Arg Tyr Thr
275 280 285

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly
290 295 300

Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Gln Lys Leu Gln
305 310 315 320

Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr Met
325 330 335

Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala
340 345 350

Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr
355 360 365

Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly
370 375 380

Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser Pro
385 390 395 400

Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
405 410 415

Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
420 425 430

Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly
435 440 445

Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu
450 455 460

Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
465 470 475 480

Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
485 490 495

Ile Lys

<210> 181
<211> 1527
<212> DNA
<213> artificial sequence

<220>
<223> antiCD19xantiCD3 VH2VL3

<400> 181
gatatccagc tgacccagtc tccagcttct ttggctgtgt ctctagggca gagggccacc 60
atctcctgca aggccagcca aagtgttgat tatgatgggtg atagttatth gaactgggtac 120
caacagattc caggacagcc acccaaactc ctcatctatg atgcatccaa tctagtttct 180
gggatcccac ccagggtttag tggcagtggtg tctgggacag acttcaccct caacatccat 240
cctgtggaga aggtggatgc tgcaacctat cactgtcagc aaagtactga ggatccgtgg 300
acgttcggtg gagggaccaa gctcgagatc aaaggtgggtg gtggttctgg cggcggcggc 360
tccggtgggtg gtggttctca ggtgcagctg cagcagtctg gggctgagct ggtgaggcct 420
gggtcctcag tgaagatttc ctgcaaggct tctggctatg cattcagtag ctactggatg 480
aactgggtga agcagaggcc tggacagggt cttgagtggg ttggacagat ttggcctgga 540
gatgggtgata ctaactacaa tggaaagtcc aagggtaaag ccactctgac tgcagacgaa 600
tcctccagca cagcctacat gcaactcagc agcctagcat ctgaggactc tgcggtctat 660
ttctgtgcaa gacgggagac tacgacggta ggccgttatt actatgctat ggactactgg 720
ggccaaggga ccacgggtcac cgtctcctcc ggaggtgggtg gctccgacgt ccaactgggtg 780
cagtcagggg ctgaagtga aaaacctggg gcctcagtga aggtgtcctg caaggcttct 840
ggctacaccg ctactaggta cacgatgcac tgggtaaggc aggcacctgg acagggtctg 900
gaatggattg gatacattha tcctagccgt gggtatacta attacgcaca gaagttgcag 960
ggccgcgtca caatgactac agacacttcc accagcacag cctacatgga actgagcagc 1020
ctgcgttctg aggacactgc aacctattac tgtgcaagat attatgatga tcattactgc 1080
cttgactact ggggccaagg caccacggtc accgtctcct caggcgaagg tactagtact 1140
ggttctgggtg gaagtggagg ttcagggtgga gcagacgaca ttgtactgac ccagtctcca 1200
gcaactctgt ctctgtctcc aggggagcgt gccaccctga cctgcagagc cagttcaagt 1260
gtaagttaca tgaactggta ccagcagaag ccgggcaagg caccctaaaag atggatttat 1320
gacacatcca aagtggcttc tggagtcctt gctcgcttca gtggcagtggt gtctgggacc 1380
gactactctc tcacaatcaa cagcttgagg gctgaagatg ctgccactta ttactgocaa 1440
cagtgagata gtaaccgct cacgttcggt ggcgggacca aggtggagat caaacatcat 1500

caccatcatc attagagatc tgtcgac

1527

<210> 182

<211> 498

<212> PRT

<213> artificial sequence

<220>

<223> antiCD19xantiCD3 VH2VL3

<400> 182

Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
20 25 30

Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65 70 75 80

Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
85 90 95

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
115 120 125

Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val
130 135 140

Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met
145 150 155 160

Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln
165 170 175

Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly

180

185

190

Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln
195 200 205

Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg
210 215 220

Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp
225 230 235 240

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp
245 250 255

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser
260 265 270

Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ala Thr Arg Tyr Thr
275 280 285

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly
290 295 300

Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Gln Lys Leu Gln
305 310 315 320

Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr Met
325 330 335

Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala
340 345 350

Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr
355 360 365

Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly
370 375 380

Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser Pro
385 390 395 400

Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys Arg
405 410 415

Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
 420 425 430

Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly
 435 440 445

Val Pro Ala Arg Phe Ser Gly Ser Gly Thr Asp Tyr Ser Leu
 450 455 460

Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
 465 470 475 480

Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
 485 490 495

Ile Lys

<210> 183
 <211> 1527
 <212> DNA
 <213> artificial sequence

<220>
 <223> antiCD19xantiCD3 VH3VL1

<400> 183
 gatatccagc tgacccagtc tccagcttct ttggctgtgt ctctagggca gagggccacc 60
 atctcctgca aggccagcca aagtgttgat tatgatgggtg atagttattt gaactgggtac 120
 caacagattc caggacagcc acccaaactc ctcatctatg atgcatccaa tctagtttct 180
 gggatcccac ccagggtttag tggcagtggg tctgggacag acttcaccct caacatccat 240
 cctgtggaga aggtggatgc tgcaacctat cactgtcagc aaagtactga ggatccgtgg 300
 acgttcggtg gagggaccaa gctcgagatc aaaggtggtg gtggttctgg cggcggcggc 360
 tccggtggtg gtggttctca ggtgcagctg cagcagtctg gggctgagct ggtgaggcct 420
 gggtcctcag tgaagatttc ctgcaaggct tctggctatg cattcagtag ctactggatg 480
 aactgggtga agcagaggcc tggacagggt cttgagtgga ttggacagat ttggcctgga 540
 gatggtgata ctaactacaa tggaaagttc aagggtaaag ccactctgac tgcagacgaa 600
 tcctccagca cagcctacat gcaactcagc agcctagcat ctgaggactc tgcggtctat 660
 ttctgtgcaa gacgggagac tacgacggta ggccgttatt actatgctat ggactactgg 720
 ggccaaggga ccacggtcac cgtctcctcc ggaggtggtg gctccgacgt ccaactggtg 780

cagtcagggg ctgaagtgaa aaaacctggg gcctcagtga aggtgtcctg caaggcttct 840
 ggctacaccg ctactaggta cacgatgcac tgggtaaggc aggcacctgg acaggggtctg 900
 gaatggattg gatacattaa tcctagccgt gggtatacta attacgcaca gaagttgcag 960
 ggccgcgtca caatgactac agacacttcc accagcacag cctacctgca aatgaacagc 1020
 ctgaaaactg aggacactgc agtctattac tgtgcaagat attatgatga tcattactgc 1080
 cttgactact ggggccaaagg caccacgggc accgtctcct caggcgaagg tactagtact 1140
 ggttctgggtg gaagtggagg ttcaggtgga gcagacgaca ttcagatgac ccagtctcca 1200
 tctagcctgt ctgcatctgt cggggaccgt gtcaccatca cctgcagagc cagtcaaagt 1260
 gtaagttaca tgaactggta ccagcagaag ccgggcaagg caccctaaaag atggatttat 1320
 gacacatcca aagtggcttc tggagtcctt gctcgcttca gtggcagtgg gtctgggacc 1380
 gactactctc tcacaatcaa cagcttggag gctgaagatg ctgccactta ttactgccaa 1440
 cagtggagta gtaaccgct cacgttcggt ggccgggacca aggtggagat caaacatcat 1500
 caccatcatc attagagatc tgtcgac 1527

<210> 184
 <211> 498
 <212> PRT
 <213> artificial sequence

<220>
 <223> antiCD19xantiCD3 VH3VL1

<400> 184

Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
 20 25 30

Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
 35 40 45

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
 65 70 75 80

Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
 85 90 95

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
115 120 125

Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val
130 135 140

Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met
145 150 155 160

Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln
165 170 175

Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly
180 185 190

Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln
195 200 205

Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg
210 215 220

Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp
225 230 235 240

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp
245 250 255

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser
260 265 270

Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ala Thr Arg Tyr Thr
275 280 285

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly
290 295 300

Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Gln Lys Leu Gln
305 310 315 320

Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr Leu

325

330

335

Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 340 345 350

Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr
 355 360 365

Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly
 370 375 380

Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser Pro
 385 390 395 400

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
 405 410 415

Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
 420 425 430

Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly
 435 440 445

Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu
 450 455 460

Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
 465 470 475 480

Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
 485 490 495

Ile Lys

<210> 185
 <211> 1527
 <212> DNA
 <213> artificial sequence

<220>
 <223> antiCD19xantiCD3 VH3VL2

<400> 185
 gatatccagc tgaccagtc tccagcttct ttggctgtgt ctctagggca gagggccacc 60
 atctcctgca aggccagcca aagtgttgat tatgatggtg atagttattt gaactggtac 120

caacagattc caggacagcc acccaaactc ctcatctatg atgcatccaa tctagtttct 180
gggatccac ccaggtttag tggcagtggg tctgggacag acttcaccct caacatccat 240
cctgtggaga aggtggatgc tgcaacctat cactgtcagc aaagtactga ggatccgtgg 300
acgttcggtg gagggaccaa gctcgagatc aaaggtggtg gtggttctgg cggcggcggc 360
tccggtggtg gtggttctca ggtgcagctg cagcagtctg gggctgagct ggtgaggcct 420
gggtcctcag tgaagatttc ctgcaaggct tctggctatg cattcagtag ctactggatg 480
aactgggtga agcagaggcc tggacagggt cttgagtgga ttggacagat ttggcctgga 540
gatggtgata ctaactacaa tggaaagttc aagggtaaag ccactctgac tgcagacgaa 600
tctccagca cagcctacat gcaactcagc agcctagcat ctgaggactc tgcggtctat 660
ttctgtgcaa gacgggagac tacgacggta ggccgttatt actatgctat ggactactgg 720
ggccaagga ccacggtcac cgtctcctcc ggaggtggtg gctccgacgt ccaactggtg 780
cagtcagggg ctgaagtga aaaacctggg gcctcagtga aggtgtcctg caaggcttct 840
ggctacaccg ctactaggta cacgatgcac tgggtaaggc aggcacctgg acagggtctg 900
gaatggattg gatacattaa tcctagccgt gggtatacta attacgcaca gaagttgcag 960
ggccgcgtca caatgactac agacacttcc accagcacag cctacctgca aatgaacagc 1020
ctgaaaactg aggacactgc agtctattac tgtgcaagat attatgatga tcattactgc 1080
cttgactact ggggccaagg caccacggtc accgtctcct caggcgaagg tactagtact 1140
ggttctggtg gaagtggagg ttcaggtgga gcagacgaca ttgtactgac ccagtctcca 1200
gcaactctgt ctctgtctcc aggggagcgt gccaccctga gctgcagagc cagtcaaagt 1260
gtaagttaca tgaactggta ccagcagaag ccgggcaagg caccctaaaag atggatttat 1320
gacacatcca aagtggcttc tggagtcctt gctcgcttca gtggcagtgg gtctgggacc 1380
gactactctc tcacaatcaa cagcttggag gctgaagatg ctgccactta ttactgcca 1440
cagtggagta gtaacccgct cacgttcggt ggccgggacca aggtggagat caaacatcat 1500
caccatcatc attagagatc tgtcgac 1527

<210> 186

<211> 498

<212> PRT

<213> artificial sequence

<220>

<223> antiCD19xantiCD3 VH3VL2

<400> 186

Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1 5 10 15
 Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
 20 25 30
 Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
 35 40 45
 Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
 50 55 60
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
 65 70 75 80
 Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
 85 90 95
 Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
 100 105 110
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
 115 120 125
 Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val
 130 135 140
 Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met
 145 150 155 160
 Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln
 165 170 175
 Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly
 180 185 190
 Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln
 195 200 205
 Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg
 210 215 220
 Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp
 225 230 235 240

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp
245 250 255

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser
260 265 270

Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ala Thr Arg Tyr Thr
275 280 285

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly
290 295 300

Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Gln Lys Leu Gln
305 310 315 320

Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr Leu
325 330 335

Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Ala
340 345 350

Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr
355 360 365

Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly
370 375 380

Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser Pro
385 390 395 400

Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
405 410 415

Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
420 425 430

Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly
435 440 445

Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu
450 455 460

Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln

Ile Lys

<400>	187					
gatatccagc	tgacccagtc	tccagcttct	ttggctgtgt	ctctagggca	gagggccacc	60
atctcctgca	aggccagcca	aagtgttgat	tatgatgggtg	atagttattt	gaactggtac	120
caacagattc	caggacagcc	acccaaactc	ctcatctatg	atgcatccaa	tctagtttct	180
gggatcccac	ccaggtttag	tggcagtggg	tctgggacag	acttcaccct	caacatccat	240
cctgtggaga	aggtggatgc	tgcaacctat	cactgtcagc	aaagtactga	ggatccgtgg	300
acgttcggtg	gagggaccaa	gctcgagatc	aaaggtgggtg	gtggttctgg	cggcggcggc	360
tccggtgggtg	gtggttctca	ggtgcagctg	cagcagttctg	gggctgagct	ggtgaggcct	420
gggtcctcag	tgaagatttc	ctgcaaggct	tctggctatg	cattcagtag	ctactggatg	480
aactgggtga	agcagaggcc	tggacagggt	cttgagtgga	ttggacagat	ttggcctgga	540
gatggtgata	ctaactacaa	tggaaagttc	aagggtaaag	ccactctgac	tgcagacgaa	600
tcctccagca	cagcctacat	gcaactcagc	agcctagcat	ctgaggactc	tgcggtctat	660
ttctgtgcaa	gacgggagac	tacgacggta	ggccgttatt	actatgctat	ggactactgg	720
ggccaaggga	ccacggtcac	cgtctcctcc	ggaggtgggtg	gctccgacgt	ccaactgggtg	780
cagtcagggg	ctgaagtgaa	aaaacctggg	gcctcagtga	aggtgtcctg	caaggcttct	840
ggctacaccg	ctactaggta	cacgatgcac	tgggtaaggc	aggcacctgg	acagggtctg	900
gaatggattg	gatacattaa	tcctagccgt	ggttatacta	attacgcaca	gaagttgcag	960
ggccgcgtca	caatgactac	agacacttcc	accagcacag	cctacctgca	aatgaacagc	1020
ctgaaaactg	aggacactgc	agtctattac	tgtgcaagat	attatgatga	tcattactgc	1080
cttgactact	ggggccaagg	caccacggtc	accgtctcct	caggcgaagg	tactagtact	1140
ggttctgggtg	gaagtggagg	ttcaggtgga	gcagacgaca	ttgtactgac	ccagttctcca	1200

gcaactctgt ctctgtctcc aggggagcgt gccaccctga cctgcagagc cagttcaagt 1260
 gtaagttaca tgaactggta ccagcagaag ccgggcaagg cacccaaaag atggatttat 1320
 gacacatcca aagtggcttc tggagtccct gctcgcttca gtggcagtgg gtctgggacc 1380
 gactactctc tcacaatcaa cagcttggag gctgaagatg ctgccactta ttactgcca 1440
 cagtggagta gtaacccgct cacgttcggt ggcgggacca aggtggagat caaacatcat 1500
 caccatcatc attagagatc tgtcgac 1527

<210> 188

<211> 498

<212> PRT

<213> artificial sequence

<220>

<223> antiCD19xantiCD3 VH3VL3

<400> 188

Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
 20 25 30

Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
 35 40 45

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
 65 70 75 80

Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
 85 90 95

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
 100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
 115 120 125

Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val
 130 135 140

Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met
 145 150 155 160

Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln
 165 170 175

Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly
 180 185 190

Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln
 195 200 205

Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg
 210 215 220

Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp
 225 230 235 240

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp
 245 250 255

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser
 260 265 270

Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ala Thr Arg Tyr Thr
 275 280 285

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly
 290 295 300

Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Gln Lys Leu Gln
 305 310 315 320

Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr Leu
 325 330 335

Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 340 345 350

Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr
 355 360 365

Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly
 370 375 380

Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser Pro
385 390 395 400

Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys Arg
405 410 415

Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
420 425 430

Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly
435 440 445

Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu
450 455 460

Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
465 470 475 480

Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
485 490 495

Ile Lys

<210> 189
<211> 1527
<212> DNA
<213> artificial sequence

<220>
<223> antiCD19xantiCD3 VH5VL1

<400> 189
gatatccagc tgaccagtc tccagcttct ttggctgtgt ctctagggca gagggccacc 60
atctcctgca aggccagcca aagtgttgat tatgatgggtg atagttattt gaactggtac 120
caacagattc caggacagcc acccaaactc ctcatctatg atgcatccaa tctagtttct 180
gggatccac ccaggttttag tggcagtggg tctgggacag acttcaccct caacatccat 240
cctgtggaga aggtggatgc tgcaacctat cactgtcagc aaagtactga ggatccgtgg 300
acgttcggtg gagggaccaa gctcgagatc aaagggtggtg gtggttctgg cggcggcggc 360
tccggtggtg gtggttctca ggtgcagctg cagcagttctg gggctgagct ggtgaggcct 420
gggtcctcag tgaagatttc ctgcaaggct tctggctatg cattcagtag ctactggatg 480

aactgggtga agcagaggcc tggacagggt cttgagtga ttggacagat ttggcctgga 540
gatggtgata ctaactacaa tggaaagttc aagggtaaag ccactctgac tgcagacgaa 600
tcctccagca cagcctacat gcaactcagc agcctagcat ctgaggactc tgcggtctat 660
ttctgtgcaa gacgggagac tacgacggta ggccgttatt actatgctat ggactactgg 720
ggccaaggga ccacggtcac cgtctcctcc ggaggtggtg gctccgacgt ccaactggtg 780
cagtcagggg ctgaagtga aaaacctggg gcctcagtga aggtgtcctg caaggcttct 840
ggctacacct ttactaggta cacgatgcac tgggtaaggc aggcacctgg acagggtctg 900
gaatggattg gatacatata tcctagccgt gggtatacta attacgcaga cagcgtcaag 960
ggccgcttca caatcactac agacaaatcc accagcacag cctacatgga actgagcagc 1020
ctgcgttctg aggacactgc aacctattac tgtgcaagat attatgatga tcattactgc 1080
cttgactact ggggccaagg caccacggtc accgtctcct caggcgaagg tactagtact 1140
ggttctggtg gaagtggagg ttcaggtgga gcagacgaca ttcagatgac ccagtctcca 1200
tctagcctgt ctgcatctgt cggggaccgt gtcaccatca cctgcagagc cagtcaaagt 1260
gtaagttaca tgaactggta ccagcagaag ccgggcaagg cacccaaaag atggatttat 1320
gacacatcca aagtggcttc tggagtccct gctcgcttca gtggcagtgg gtctgggacc 1380
gactactctc tcacaatcaa cagcttggag gctgaagatg ctgccactta ttactgcca 1440
cagtggagta gtaacccgct cacgttcggt ggcgggacca aggtggagat caaacatcat 1500
caccatcatc attagagatc tgtcgac 1527

<210> 190

<211> 498

<212> PRT

<213> artificial sequence

<220>

<223> antiCD19xantiCD3 VH5VL1

<400> 190

Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
20 25 30

Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
 65 70 75 80

Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
 85 90 95

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
 100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
 115 120 125

Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val
 130 135 140

Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met
 145 150 155 160

Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln
 165 170 175

Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly
 180 185 190

Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln
 195 200 205

Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg
 210 215 220

Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp
 225 230 235 240

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp
 245 250 255

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser
 260 265 270

Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr
 275 280 285

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly
290 295 300

Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys
305 310 315 320

Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met
325 330 335

Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala
340 345 350

Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr
355 360 365

Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly
370 375 380

Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser Pro
385 390 395 400

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
405 410 415

Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
420 425 430

Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly
435 440 445

Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu
450 455 460

Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
465 470 475 480

Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
485 490 495

Ile Lys

<210> 191
<211> 1527

<212> DNA

<213> artificial sequence

<220>

<223> antiCD19xantiCD3 VH5VL2

<400> 191

gatatccagc tgacccagtc tccagcttct ttggctgtgt ctctagggca gagggccacc	60
atctcctgca aggccagcca aagtgttgat tatgatgggtg atagtatttt gaactgggtac	120
caacagattc caggacagcc acccaaactc ctcatctatg atgcatccaa tctagtttct	180
gggatccac ccaggtttag tggcagtggg tctgggacag acttcaccct caacatccat	240
cctgtggaga aggtggatgc tgcaacctat cactgtcagc aaagtactga ggatccgtgg	300
acgttcgggtg gagggaccaaa gctcgagatc aaagggtgggtg gtggtttctgg cggcggcggc	360
tccgggtgggtg gtggtttctca ggtgcagctg cagcagctctg gggctgagct ggtgaggcct	420
gggtcctcag tgaagatttc ctgcaaggct tctggctatg cattcagtag ctactggatg	480
aactgggtga agcagaggcc tggacagggt cttgagtgga ttggacagat ttggcctgga	540
gatgggtgata ctaactacaa tggaaagttc aagggttaaag ccactctgac tgcagacgaa	600
tcctccagca cagcctacat gcaactcagc agcctagcat ctgaggactc tgcggtctat	660
ttctgtgcaa gacgggagac tacgacggta ggccgttatt actatgctat ggactactgg	720
ggccaaggga ccacggtcac cgtctcctcc ggaggtgggtg gctccgacgt ccaactgggtg	780
cagtcagggg ctgaagtga aaaacctggg gcctcagtga aggtgtcctg caaggcttct	840
ggctacacct ttactaggta cacgatgcac tgggtaaggc aggcacctgg acagggtctg	900
gaatggattg gatacattaa tcctagccgt gggtatacta attacgcaga cagcgtcaag	960
ggccgcttca caatcactac agacaaatcc accagcacag cctacatgga actgagcagc	1020
ctgcgttctg aggacactgc aacctattac tgtgcaagat attatgatga tcattactgc	1080
cttgactact ggggccaagg caccacggtc accgtctcct caggcgaagg tactagtact	1140
ggttctgggtg gaagtggagg ttcagggtgga gcagacgaca ttgtactgac ccagtctcca	1200
gcaactctgt ctctgtctcc aggggagcgt gccaccctga gctgcagagc cagtcaaagt	1260
gtaagttaca tgaactggta ccagcagaag ccgggcaagg caccctaaaag atggatttat	1320
gacacatcca aagtggcttc tggagtccct gctcgcttca gtggcagtgg gtctgggacc	1380
gactactctc tcacaatcaa cagcttggag gctgaagatg ctgccactta ttactgcca	1440
cagtggagta gtaacccgct cacgttcgggt ggcgggacca aggtggagat caaacatcat	1500
caccatcatc attagagatc tgtogac	1527

<210> 192
<211> 498
<212> PRT
<213> artificial sequence

<220>
<223> antiCD19xantiCD3 VH5VL2

<400> 192

Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
20 25 30

Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65 70 75 80

Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
85 90 95

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
115 120 125

Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val
130 135 140

Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met
145 150 155 160

Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln
165 170 175

Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly
180 185 190

Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln
195 200 205

Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg
210 215 220

Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp
225 230 235 240

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp
245 250 255

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser
260 265 270

Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr
275 280 285

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly
290 295 300

Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys
305 310 315 320

Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met
325 330 335

Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala
340 345 350

Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr
355 360 365

Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly
370 375 380

Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser Pro
385 390 395 400

Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
405 410 415

Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
420 425 430

Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly
435 440 445

Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu
450 455 460

Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
465 470 475 480

Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
485 490 495

Ile Lys

<210> 193
<211> 1527
<212> DNA
<213> artificial sequence

<220>
<223> antiCD19xantiCD3 VH5VL3

<400> 193
gatatccagc tgacccagtc tccagcttct ttggctgtgt ctctagggca gagggccacc 60
atctcctgca aggccagcca aagtgttgat tatgatgggtg atagttatatt gaactgggtac 120
caacagattc caggacagcc acccaaactc ctcatctatg atgcatccaa tctagtttct 180
gggatccac ccaggtttag tggcagtggg tctgggacag acttcaccct caacatccat 240
cctgtggaga aggtggatgc tgcaacctat cactgtcagc aaagtactga ggatccgtgg 300
acgttcggtg gagggaccaa gctcgagatc aaaggtgggtg gtggttcttg cggcggcggc 360
tccggtggtg gtggttctca ggtgcagctg cagcagtctg gggctgagct ggtgaggcct 420
gggtcctcag tgaagatttc ctgcaaggct tctggctatg cattcagtag ctactggatg 480
aactgggtga agcagaggcc tggacagggt cttgagtgga ttggacagat ttggcctgga 540
gatggtgata ctaactacaa tggaaagttc aagggtaaag ccactctgac tgcagacgaa 600
tcctccagca cagcctacat gcaactcagc agcctagcat ctgaggactc tgcggtctat 660
ttctgtgcaa gacgggagac tacgacggta ggccggttatt actatgctat ggactactgg 720
ggccaaggga ccacggtcac cgtctcctcc ggaggtgggtg gctccgacgt ccaactgggtg 780
cagtcagggg ctgaagtga aaaacctggg gcctcagtga aggtgtcctg caaggcttct 840
ggctacacct ttactaggta cacgatgcac tgggtaaggc aggcacctgg acagggtctg 900


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gaatggattg gatacattaa tcctagccgt gggtatacta attacgcaga cagcgtcaag      960
ggccgcttca caatcactac agacaaatcc accagcacag cctacatgga actgagcagc      1020
ctgcgttctg aggacactgc aacctattac tgtgcaagat attatgatga tcattactgc      1080
cttgactact ggggccaagg caccacggtc accgtctcct caggcgaagg tactagtact      1140
ggttctgggtg gaagtggagg ttcaggtgga gcagacgaca ttgtactgac ccagtctcca      1200
gcaactctgt ctctgtctcc aggggagcgt gccaccctga cctgcagagc cagttcaagt      1260
gtaagttaca tgaactggta ccagcagaag ccgggcaagg cacccaaaag atggatttat      1320
gacacatcca aagtggcttc tggagtcctt gctcgcttca gtggcagtgg gtctgggacc      1380
gactactctc tcacaatcaa cagcttggag gctgaagatg ctgccactta ttactgcca      1440
cagtggagta gtaaccgct caggttcggt ggcgggacca aggtggagat caaacatcat      1500
caccatcatc attagagatc tgtcgac                                     1527

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<210> 194
<211> 498
<212> PRT
<213> artificial sequence

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<220>
<223> antiCD19xantiCD3 VH5VL3

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<400> 194

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Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1           5           10           15

```

```

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
          20           25           30

```

```

Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
          35           40           45

```

```

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
          50           55           60

```

```

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65           70           75           80

```

```

Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
          85           90           95

```

```

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly

```

100	105	110
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val 115 120 125		
Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val 130 135 140		
Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met 145 150 155 160		
Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln 165 170 175		
Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly 180 185 190		
Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln 195 200 205		
Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg 210 215 220		
Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp 225 230 235 240		
Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp 245 250 255		
Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser 260 265 270		
Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr 275 280 285		
Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly 290 295 300		
Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys 305 310 315 320		
Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met 325 330 335		

Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala
 340 345 350

Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr
 355 360 365

Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly
 370 375 380

Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser Pro
 385 390 395 400

Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys Arg
 405 410 415

Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
 420 425 430

Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly
 435 440 445

Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu
 450 455 460

Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
 465 470 475 480

Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
 485 490 495

Ile Lys

<210> 195
 <211> 1527
 <212> DNA
 <213> artificial sequence

<220>
 <223> antiCD19xantiCD3 VH7VL1

<400> 195
 gatatccagc tgacccagtc tccagcttct ttggctgtgt ctctagggca gagggccacc 60
 atctcctgca aggccagcca aagtgttgat tatgatgggtg atagttatatt gaactgggtac 120
 caacagattc caggacagcc acccaaactc ctcatctatg atgcatccaa tctagtttct 180

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gggatccac ccaggttttag tggcagtggg tctgggacag acttcaccct caacatccat 240
cctgtggaga aggtggatgc tgcaacctat cactgtcagc aaagtactga ggatccgtgg 300
acgttcggtg gagggaccaa gctcgagatc aaaggtggtg gtggttctgg cggcggcggc 360
tccggtggtg gtggttctca ggtgcagctg cagcagtctg gggctgagct ggtgaggcct 420
gggtcctcag tgaagatttc ctgcaaggct tctggctatg cattcagtag ctactggatg 480
aactgggtga agcagaggcc tggacagggt cttgagtgga ttggacagat ttggcctgga 540
gatggtgata ctaactacaa tggaaagttc aagggtaaag ccactctgac tgcagacgaa 600
tcctccagca cagcctacat gcaactcagc agcctagcat ctgaggactc tgcggtctat 660
ttctgtgcaa gacgggagac tacgacggta ggccgttatt actatgctat ggactactgg 720
ggccaaggga ccacggtcac cgtctcctcc ggaggtggtg gctccgacgt ccaactggtg 780
cagtcagggg ctgaagtga aaaacctggg gcctcagtga aggtgtcctg caaggcttct 840
ggctacacct ttactaggtg cacgatgcac tgggtaaggc aggcacctgg acagggtctg 900
gaatggattg gatacatcaa tcctagccgt gggtatacta attacaatca gaagttcaag 960
gaccgcgtca caatcactac agacaaatcc accagcacag cctacatgga actgagcagc 1020
ctgcgttctg aggacactgc agtctattac tgtgcaagat attatgatga tcattactgc 1080
cttgactact ggggccaagg caccacggtc accgtctcct caggcgaagg tactagtact 1140
ggttctggtg gaagtggagg ttcagggtgga gcagacgaca ttcagatgac ccagtctcca 1200
tctagcctgt ctgcatctgt cggggaccgt gtcaccatca cctgcagagc cagtcaaagt 1260
gtaagttaca tgaactggta ccagcagaag ccgggcaagg cacccaaaag atggatttat 1320
gacacatcca aagtggcttc tggagtcctt gctcgcttca gtggcagtgg gtctgggacc 1380
gactactctc tcacaatcaa cagcttggag gctgaagatg ctgccactta ttactgcaa 1440
cagtggagta gtaacccgct cacgttcggt ggcgggacca aggtggagat caaacatcat 1500
caccatcatc attagagatc tgtcgac 1527

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<210> 196

<211> 498

<212> PRT

<213> artificial sequence

<220>

<223> antiCD19xantiCD3 VH7VL1

<400> 196

Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
20 25 30

Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65 70 75 80

Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
85 90 95

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
115 120 125

Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val
130 135 140

Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met
145 150 155 160

Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln
165 170 175

Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly
180 185 190

Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln
195 200 205

Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg
210 215 220

Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp
225 230 235 240

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp

245	250	255
Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser		
260	265	270
Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr		
275	280	285
Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly		
290	295	300
Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys		
305	310	315
Asp Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met		
325	330	335
Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala		
340	345	350
Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr		
355	360	365
Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly		
370	375	380
Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser Pro		
385	390	395
Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg		
405	410	415
Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly		
420	425	430
Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly		
435	440	445
Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu		
450	455	460
Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln		
465	470	475
		480

Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
 485 490 495

Ile Lys

<210> 197
 <211> 1527
 <212> DNA
 <213> artificial sequence

<220>
 <223> antiCD19xantiCD3 VH7VL2

<400> 197
 gatatccagc tgacccagtc tccagcttct ttggctgtgt ctctagggca gagggccacc 60
 atctcctgca aggccagcca aagtgttgat tatgatgggtg atagtatttt gaactgggtac 120
 caacagattc caggacagcc acccaaactc ctcatctatg atgcatccaa tctagtttct 180
 gggatcccac ccaggtttag tggcagtggtg tctgggacag acttcaccct caacatccat 240
 cctgtggaga aggtggatgc tgcaacctat cactgtcagc aaagtactga ggatccgtgg 300
 acgttcggtg gagggaccaa gctcgagatc aaaggtgggtg gtggttcttg cggcggcggc 360
 tccggtgggtg gtggttctca ggtgcagctg cagcagctctg gggctgagct ggtgaggcct 420
 gggtcctcag tgaagatttc ctgcaaggct tctggctatg cattcagtag ctactggatg 480
 aactgggtga agcagaggcc tggacagggt cttgagtgga ttggacagat ttggcctgga 540
 gatgggtgata ctaactacaa tggaaagttc aagggttaaag ccactctgac tgcagacgaa 600
 tcctccagca cagcctacat gcaactcagc agcctagcat ctgaggactc tgcggtctat 660
 ttctgtgcaa gacgggagac tacgacggta ggccgttatt actatgctat ggactactgg 720
 ggccaaggga ccacggtcac cgtctcctcc ggagggtgggtg gctccgacgt ccaactgggtg 780
 cagtcagggg ctgaagtga aaaacctggg gcctcagtga aggtgtcctg caaggcttct 840
 ggctacacct ttactaggta cacgatgcac tgggtaaggc aggcacctgg acagggtctg 900
 gaatggattg gatacatata tcctagccgt gggtatacta attacaatca gaagttcaag 960
 gaccgcgtca caatcactac agacaaatcc accagcacag cctacatgga actgagcagc 1020
 ctgcgttctg aggacactgc agtctattac tgtgcaagat attatgatga tcattactgc 1080
 cttgactact ggggccaagg caccacggtc accgtctcct caggcgaagg tactagtact 1140
 ggttctgggtg gaagtggagg ttcagggtgga gcagacgaca ttgtactgac ccagtctcca 1200
 gcaactctgt ctctgtctcc aggggagcgt gccacctga gctgcagagc cagtcaaagt 1260

gtaagttaca tgaactggta ccagcagaag ccgggcaagg cacccaaaag atggatttat 1320
gacacatcca aagtggcttc tggagtcctt gctcgttca gtggcagtgg gtctgggacc 1380
gactactctc tcacaatcaa cagcttggag gctgaagatg ctgccactta ttactgccaa 1440
cagtggagta gtaacccgct cacgttcggt ggcgggacca aggtggagat caaacatcat 1500
caccatcatc attagagatc tgtcgac 1527

<210> 198
<211> 498
<212> PRT
<213> artificial sequence

<220>
<223> antiCD19xantiCD3 VH7VL2

<400> 198

Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
20 25 30

Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65 70 75 80

Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
85 90 95

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
115 120 125

Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val
130 135 140

Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met
145 150 155 160

Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln
 165 170 175

Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly
 180 185 190

Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln
 195 200 205

Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg
 210 215 220

Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp
 225 230 235 240

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp
 245 250 255

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser
 260 265 270

Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr
 275 280 285

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly
 290 295 300

Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys
 305 310 315 320

Asp Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met
 325 330 335

Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 340 345 350

Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr
 355 360 365

Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly
 370 375 380

Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser Pro

<400> 199						
gatatccagc	tgacccagtc	tccagcttct	ttggctgtgt	ctctagggca	gagggccacc	60
atctcctgca	aggccagcca	aagtgttgat	tatgatgggtg	atagttat	gaactggtag	120
caacagattc	caggacagcc	acccaaactc	ctcatctatg	atgcatccaa	tctagtttct	180
gggatcccac	ccaggtttag	tggcagtggtg	tctgggacag	acttcaccct	caacatccat	240
cctgtggaga	aggtggatgc	tgcaacctat	cactgtcagc	aaagtactga	ggatccgtgg	300
acgttcggtg	gagggaccaa	gctcgagatc	aaaggtgggtg	gtggttctgg	cggcgggcggc	360
tccggtgggtg	gtggttctca	ggtgcagctg	cagcagtcctg	gggctgagct	ggtgaggcct	420
gggtcctcag	tgaagatttc	ctgcaaggct	tctggctatg	cattcagtag	ctactggatg	480
aactgggtga	agcagaggcc	tggacaggggt	cttgagtggg	ttggacagat	ttggcctgga	540
gatgggtgata	ctaactacaa	tggaaagtgc	aagggttaaag	ccactctgac	tgcagacgaa	600

tcctccagca cagcctacat gcaactcagc agcctagcat ctgaggactc tgcggtctat 660
ttctgtgcaa gacgggagac tacgacggta ggccgttatt actatgctat ggactactgg 720
ggccaaggga ccacggtcac cgtctcctcc ggaggtggtg gctccgacgt ccaactggtg 780
cagtcagggg ctgaagtga aaaacctggg gcctcagtga aggtgtcctg caaggcttct 840
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gaatggattg gatacattaa tcctagccgt gggtatacta attacaatca gaagttcaag 960
gaccgcgtca caatcactac agacaaatcc accagcacag cctacatgga actgagcagc 1020
ctgcgttctg aggacactgc agtctattac tgtgcaagat attatgatga tcattactgc 1080
cttgactact ggggccaagg caccacggtc accgtctcct caggcgaagg tactagtact 1140
ggttctggtg gaagtggagg ttcaggtgga gcagacgaca ttgtactgac ccagtctcca 1200
gcaactctgt ctctgtctcc aggggagcgt gccaccctga cctgcagagc cagttcaagt 1260
gtaagttaca tgaactggta ccagcagaag ccgggcaagg cacccaaaag atggatttat 1320
gacacatcca aagtggcttc tggagtcctt gctcgcttca gtggcagtgg gtctgggacc 1380
gactactctc tcacaatcaa cagcttggag gctgaagatg ctgccactta ttactgcca 1440
cagtggagta gtaaccgct cacgttcggt ggcgggacca aggtggagat caaacatcat 1500
caccatcatc attagagatc tgtcgac 1527

<210> 200
<211> 498
<212> PRT
<213> artificial sequence

<220>
<223> antiCD19xantiCD3 VH7VL3

<400> 200

Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
20 25 30

Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65 70 75 80

Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
85 90 95

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
115 120 125

Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val
130 135 140

Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met
145 150 155 160

Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln
165 170 175

Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly
180 185 190

Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln
195 200 205

Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg
210 215 220

Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp
225 230 235 240

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp
245 250 255

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser
260 265 270

Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr
275 280 285

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly
290 295 300

Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys
305 310 315 320

Asp Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met
325 330 335

Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
340 345 350

Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr
355 360 365

Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly
370 375 380

Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser Pro
385 390 395 400

Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys Arg
405 410 415

Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
420 425 430

Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly
435 440 445

Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu
450 455 460

Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
465 470 475 480

Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
485 490 495

Ile Lys

<210> 201

<211> 45

<212> DNA

<213> artificial sequence

<220>

<223> standard linker

<400> 201

ggtaggtggtag gttctggcgg cggcggctcc ggtggtaggtg gttct

45

<210> 202

<211> 54

<212> DNA

<213> artificial sequence

<220>

<223> deimmunized linker

<400> 202

ggcgaaggta ctagtactgg ttctggtagga agtggaggtt caggtaggagc agac

54

<210> 203

<211> 1494

<212> DNA

<213> artificial sequence

<220>

<223> antiCD19xantiCD3

<400> 203

gatatccagc tgacccagtc tccagcttct ttggctgtgt ctctagggca gagggccacc 60

atctcctgca aggccagcca aagtgttgat tatgatggtag atagtatttt gaactggtag 120

caacagattc caggacagcc acccaaactc ctcatctatg atgcatccaa tctagtttct 180

gggatccac ccaggtttag tggcagtggt tctgggacag acttcaccct caacatccat 240

cctgtggaga aggtggatgc tgcaacctat cactgtcagc aaagtactga ggatccgtgg 300

acgttcggtag gagggaccaa gctcagagatc aaaggtaggtg gtggttctgg cggcggcggc 360

tccggtaggtg gtggttctca ggtgcagctg cagcagctctg gggctgagct ggtgaggcct 420

gggtcctcag tgaagatttc ctgcaaggct tctggctatg cattcagtag ctactggatg 480

aactgggtga agcagaggcc tggacagggt cttgagtgga ttggacagat ttggcctgga 540

gatggtagata ctaactacaa tggaaagttc aagggttaaag ccactctgac tgcagacgaa 600

tcctccagca cagcctacat gcaactcagc agcctagcat ctgaggactc tgcggtctat 660

ttctgtgcaa gacgggagac tacgacggta ggccgttatt actatgctat ggactactgg 720

ggccaaggga ccacggtcac cgtctcctcc ggaggtaggtg gatccgatat caaactgcag 780

cagtcagggg ctgaactggc aagacctggg gcctcagtga agatgtcctg caagacttct 840

ggctacacct ttactaggta cacgatgcac tgggtaaaac agaggcctgg acagggtctg 900

gaatggattg gatacatcaa tcctagccgt gggtatacta attacatca gaagttcaag 960

gacaaggcca cattgactac agacaaatcc tccagcacag cctacatgca actgagcagc 1020
 ctgacatctg aggactctgc agtctattac tgtgcaagat attatgatga tcattactgc 1080
 cttgactact ggggccaagg caccactctc acagtctcct cagtcgaagg tggaagtgga 1140
 ggttctgggtg gaagtggagg ttcaggtgga gtcgacgaca ttcagctgac ccagtctcca 1200
 gcaatcatgt ctgcatctcc aggggagaag gtcaccatga cctgcagagc cagttcaagt 1260
 gtaagttaca tgaactggta ccagcagaag tcaggcacct cccccaag atggatttat 1320
 gacacatcca aagtggcttc tggagtcctt tatcgcttca gtggcagtggt gtctgggacc 1380
 tcatactctc tcacaatcag cagcatggag gctgaagatg ctgccactta ttactgcca 1440
 cagtggagta gtaacccgct cacgttcggt gctgggacca agctggagct gaaa 1494

<210> 204
 <211> 498
 <212> PRT
 <213> artificial sequence

<220>
 <223> antiCD19xantiCD3

<400> 204

Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
 20 25 30

Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
 35 40 45

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
 65 70 75 80

Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
 85 90 95

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
 100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val

115

120

125

Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val
 130 135 140

Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met
 145 150 155 160

Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln
 165 170 175

Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly
 180 185 190

Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln
 195 200 205

Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg
 210 215 220

Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp
 225 230 235 240

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp
 245 250 255

Ile Lys Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser
 260 265 270

Val Lys Met Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Arg Tyr Thr
 275 280 285

Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly
 290 295 300

Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys
 305 310 315 320

Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr Met
 325 330 335

Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala
 340 345 350

Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr
 355 360 365

Thr Leu Thr Val Ser Ser Val Glu Gly Gly Ser Gly Gly Ser Gly Gly
 370 375 380

Ser Gly Gly Ser Gly Gly Val Asp Asp Ile Gln Leu Thr Gln Ser Pro
 385 390 395 400

Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg
 405 410 415

Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly
 420 425 430

Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly
 435 440 445

Val Pro Tyr Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu
 450 455 460

Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
 465 470 475 480

Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu
 485 490 495

Leu Lys

<210> 205
 <211> 1476
 <212> DNA
 <213> artificial sequence

<220>
 <223> CCR5xanti-CD3 VH5VL1

<400> 205
 gacattatcc tgateccaatc tccaccttct ttggctgtgt ctctagggca gagggccacc 60
 atctcctgca gaaccagoga aaatggtgac ggatacggca ttagttttat aaactggtac 120
 caacagaagc caggacagcc acccaaactc ctcatctatg ctgcatccca ccaaggatcc 180
 ggggtccctg ccagatttag tggcagtggg tctgggacag acttcagcct caacatccat 240
 cctttggagg aggatgatac tgcaatgtat ttctgtcacc aaagtaagaa gggtccgtgg 300

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acgttcggtg gaggcaccaa gctggaaatc aaaggtggtg gtggttctgg cggcggcggc 360
tccggtggtg gtggttctca gctggagcag tctggacctg aactgaagaa gcctggagag 420
acagtcacga tctcctgcaa ggcttctggg tataccttca cgaagttcgg aatgaactgg 480
gtgaagcagg ctccaggaaa gggtttaaag tggatgggct ggatacacac ctccactgga 540
gagccaacat attctgatga cttcaaggga cggtttgcct tctctttgga aacgtctgcc 600
agcactgcct atttgcggat caacaacctc aaaaatgagg acatggctaa atacttctgt 660
gccagaggtg gtccttacgt aaggggtgct ttggactact ggggtcaagg aacctcagtc 720
accgtctcct ccggaggtgg tggatccgac gtccaactgg tgcagtcagg ggctgaagtg 780
aaaaaacctg gggcctcagt gaaggtgtcc tgcaaggctt ctggctacac ctttactagg 840
tacacgatgc actgggtaag gcaggcacct ggacagggtc tggaatggat tggatacatt 900
aatcctagcc gtggttatac taattacgca gacagcgtca agggccgctt cacaatcact 960
acagacaaat ccaccagcac agcctacatg gaactgagca gcctgcgttc tgaggacact 1020
gcaacctatt actgtgcaag atattatgat gatcattact gccttgacta ctggggccaa 1080
ggcaccacgg tcaccgtctc ctcaggcgaa ggtactagta ctggttctgg tggaagtgga 1140
ggttcaggtg gagcagacga cattcagatg acccagtctc catctagcct gtctgcatct 1200
gtcgggggacc gtgtcaccat cacctgcaga gccagtcaaa gtgtaagtta catgaactgg 1260
taccagcaga agccggggcaa ggcacccaaa agatggattt atgacacatc caaagtggct 1320
tctggagtcc ctgctcgctt cagtggcagt gggctctggga ccgactactc tctcacaatc 1380
aacagcttgg aggctgaaga tgctgccact tattactgcc aacagtggag tagtaacccg 1440
ctcacgttcg gtggcgggac caaggtggag atcaaa 1476

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<210> 206

<211> 492

<212> PRT

<213> artificial sequence

<220>

<223> CCR5xanti-CD3 VH5VL1

<400> 206

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Asp Ile Ile Leu Ile Gln Ser Pro Pro Ser Leu Ala Val Ser Leu Gly
1           5           10          15

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Gln Arg Ala Thr Ile Ser Cys Arg Thr Ser Glu Asn Val Asp Gly Tyr
          20          25          30

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Gly Ile Ser Phe Ile Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45

Lys Leu Leu Ile Tyr Ala Ala Ser His Gln Gly Ser Gly Val Pro Ala
 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Asn Ile His
 65 70 75 80

Pro Leu Glu Glu Asp Asp Thr Ala Met Tyr Phe Cys His Gln Ser Lys
 85 90 95

Lys Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
 100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Leu
 115 120 125

Glu Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu Thr Val Thr Ile
 130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Lys Phe Gly Met Asn Trp
 145 150 155 160

Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met Gly Trp Ile His
 165 170 175

Thr Ser Thr Gly Glu Pro Thr Tyr Ser Asp Asp Phe Lys Gly Arg Phe
 180 185 190

Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr Leu Arg Ile Asn
 195 200 205

Asn Leu Lys Asn Glu Asp Met Ala Lys Tyr Phe Cys Ala Arg Gly Gly
 210 215 220

Pro Tyr Val Arg Gly Ala Leu Asp Tyr Trp Gly Gln Gly Thr Ser Val
 225 230 235 240

Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Val Gln Leu Val Gln Ser
 245 250 255

Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys
 260 265 270

Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln
275 280 285

Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg
290 295 300

Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Thr
305 310 315 320

Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg
325 330 335

Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His
340 345 350

Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
355 360 365

Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly
370 375 380

Ala Asp Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
385 390 395 400

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser
405 410 415

Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp
420 425 430

Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser
435 440 445

Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu
450 455 460

Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro
465 470 475 480

Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
485 490

<210> 207

<211> 1476

<212> DNA

<213> artificial sequence

<220>

<223> CCR5xanti-CD3 VH5VL2

<400> 207

gacattatcc tgatccaatc tccaccttct ttggctgtgt ctctagggca gagggccacc	60
atctcctgca gaaccagcga aaatgttgac ggatacggca ttagttttat aaactggtac	120
caacagaagc caggacagcc acccaaactc ctcatctatg ctgcatccca ccaaggatcc	180
ggggtccctg ccagatttag tggcagtggg tctgggacag acttcagcct caacatccat	240
cctttggagg aggatgatac tgcaatgtat ttctgtcacc aaagtaagaa ggttccgtgg	300
acgttcggtg gaggcaccaa gctggaaatc aaaggtggtg gtggttctgg cggcggcggc	360
tccggtggtg gtggttctca gctggagcag tctggacctg aactgaagaa gcctggagag	420
acagtcacga tctcctgcaa ggcttctggg tataccttca cgaagttcgg aatgaactgg	480
gtgaagcagg ctccaggaaa gggtttaaag tggatgggct ggatacacac ctccactgga	540
gagccaacat attctgatga cttcaaggga cggtttgcct tctctttgga aacgtctgcc	600
agcactgcct atttgcgat caacaacctc aaaaatgagg acatggctaa atacttctgt	660
gccagagggtg gtccttacgt aaggggtgct ttggactact ggggtcaagg aacctcagtc	720
accgtctcct ccggagggtg tggatccgac gtccaactgg tgcagtcagg ggctgaagtg	780
aaaaaacctg gggcctcagt gaaggtgtcc tgcaaggctt ctggctacac ctttactagg	840
tacacgatgc actgggtaag gcaggcacct ggacagggtc tggaatggat tggatacatt	900
aatcctagcc gtggttatac taattacgca gacagcgtca agggccgctt cacaatcact	960
acagacaaat ccaccagcac agcctacatg gaactgagca gcctgcgttc tgaggacact	1020
gcaacctatt actgtgcaag atattatgat gatcattact gccttgacta ctggggccaa	1080
ggcacccacgg tcaccgtctc ctcaggcgaa ggtactagta ctggttctgg tggaaagtga	1140
ggttcagggtg gagcagacga cattgtactg acccagtctc cagcaactct gtctctgtct	1200
ccaggggagc gtgccaccct gagctgcaga gccagtcaaa gtgtaagtta catgaactgg	1260
taccagcaga agccgggcaa ggcacccaaa agatggattt atgacacatc caaagtggct	1320
tctggagtcc ctgctcgctt cagtggcagt gggctctggga ccgactactc tctcacaatc	1380
aacagcttgg aggctgaaga tgctgccact tattactgcc aacagtggag tagtaacccg	1440
ctcacgttcg gtggcggggac caaggtggag atcaaa	1476

<210> 208

<211> 492
<212> PRT
<213> artificial sequence

<220>
<223> CCR5xanti-CD3 VH5VL2

<400> 208

Asp Ile Ile Leu Ile Gln Ser Pro Pro Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Arg Thr Ser Glu Asn Val Asp Gly Tyr
20 25 30

Gly Ile Ser Phe Ile Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Ala Ala Ser His Gln Gly Ser Gly Val Pro Ala
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Asn Ile His
65 70 75 80

Pro Leu Glu Glu Asp Asp Thr Ala Met Tyr Phe Cys His Gln Ser Lys
85 90 95

Lys Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Leu
115 120 125

Glu Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu Thr Val Thr Ile
130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Lys Phe Gly Met Asn Trp
145 150 155 160

Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met Gly Trp Ile His
165 170 175

Thr Ser Thr Gly Glu Pro Thr Tyr Ser Asp Asp Phe Lys Gly Arg Phe
180 185 190

Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr Leu Arg Ile Asn
195 200 205

Asn Leu Lys Asn Glu Asp Met Ala Lys Tyr Phe Cys Ala Arg Gly Gly
210 215 220

Pro Tyr Val Arg Gly Ala Leu Asp Tyr Trp Gly Gln Gly Thr Ser Val
225 230 235 240

Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Val Gln Leu Val Gln Ser
245 250 255

Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys
260 265 270

Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln
275 280 285

Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg
290 295 300

Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Thr
305 310 315 320

Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg
325 330 335

Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His
340 345 350

Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
355 360 365

Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly
370 375 380

Ala Asp Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser
385 390 395 400

Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser
405 410 415

Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp
420 425 430

Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser

435

440

445

Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu
450 455 460

Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro
465 470 475 480

Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
485 490

<210> 209

<211> 1476

<212> DNA

<213> artificial sequence

<220>

<223> CCR5xanti-CD3 VH5VL3

<400> 209

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atctcctgca gaaccagcga aaatgttgac ggatacggca ttagttttat aaactggtac 120

caacagaagc caggacagcc acccaaactc ctcatctatg ctgcatccca ccaaggatcc 180

ggggtccttg ccagatttag tggcagtggg tctgggacag acttcagcct caacatccat 240

cctttggagg aggatgatac tgcaatgtat ttctgtcacc aaagtaagaa ggttccgtgg 300

acgttcggtg gaggcaccaa gctggaaatc aaaggtggtg gtggttctgg cggcggcggc 360

tccggtggtg gtggttctca gctggagcag tctggacctg aactgaagaa gcctggagag 420

acagtcacga tctcctgcaa ggcttctggg tataccttca cgaagttcgg aatgaactgg 480

gtgaagcagg ctccaggaaa gggtttaaag tggatgggct ggatacacac ctccactgga 540

gagccaacat attctgatga cttcaaggga cggtttgctt tctctttgga aacgtctgcc 600

agcactgcct atttgcggat caacaacctc aaaaatgagg acatggctaa atacttctgt 660

gccagaggtg gtccttacgt aaggggtgct ttggactact ggggtcaagg aacctcagtc 720

accgtctcct ccggagggtg tggatccgac gtccaactgg tgcagtcagg ggctgaagtg 780

aaaaaacctg gggcctcagt gaaggtgtcc tgcaaggctt ctggctacac ctttactagg 840

tacacgatgc actgggtaag gcaggcacct ggacagggtc tggaatggat tggatacatt 900

aatcctagcc gtggttatac taattacgca gacagcgtca agggccgctt cacaatcact 960

acagacaaat ccaccagcac agcctacatg gaactgagca gcctgcgttc tgaggacact 1020

gcaacctatt actgtgcaag atattatgat gatcattact gccttgacta ctggggccaa 1080

ggcaccacgg tcaccgtctc ctcaggcgaa ggtactagta ctggttctgg tggaagtgga 1140
 ggttcaggtg gagcagacga cattgtactg acccagtctc cagcaactct gtctctgtct 1200
 ccaggggagc gtgccaccct gacctgcaga gccagttcaa gtgtaagtta catgaactgg 1260
 taccagcaga agccgggcaa ggcacccaaa agatggattt atgacacatc caaagtggct 1320
 tctggagtcc ctgctcgctt cagtggcagt gggctctggga ccgactactc tctcacaatc 1380
 aacagcttgg aggctgaaga tgctgccact tattactgcc aacagtggag tagtaaccgc 1440
 ctcacgttcg gtggcgggac caaggtggag atcaaa 1476

<210> 210
 <211> 492
 <212> PRT
 <213> artificial sequence

<220>
 <223> CCR5xanti-CD3 VH5VL3

<400> 210

Asp Ile Ile Leu Ile Gln Ser Pro Pro Ser Leu Ala Val Ser Leu Gly
 1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Arg Thr Ser Glu Asn Val Asp Gly Tyr
 20 25 30

Gly Ile Ser Phe Ile Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45

Lys Leu Leu Ile Tyr Ala Ala Ser His Gln Gly Ser Gly Val Pro Ala
 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Asn Ile His
 65 70 75 80

Pro Leu Glu Glu Asp Asp Thr Ala Met Tyr Phe Cys His Gln Ser Lys
 85 90 95

Lys Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
 100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Leu
 115 120 125

Glu Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu Thr Val Thr Ile

130		135		140											
Ser 145	Cys	Lys	Ala	Ser	Gly 150	Tyr	Thr	Phe	Thr	Lys 155	Phe	Gly	Met	Asn	Trp 160
Val	Lys	Gln	Ala	Pro 165	Gly	Lys	Gly	Leu	Lys 170	Trp	Met	Gly	Trp	Ile	His 175
Thr	Ser	Thr	Gly 180	Glu	Pro	Thr	Tyr	Ser 185	Asp	Asp	Phe	Lys	Gly 190	Arg	Phe
Ala	Phe	Ser	Leu	Glu	Thr	Ser	Ala 200	Ser	Thr	Ala	Tyr	Leu 205	Arg	Ile	Asn
Asn	Leu 210	Lys	Asn	Glu	Asp	Met	Ala 215	Lys	Tyr	Phe	Cys	Ala 220	Arg	Gly	Gly
Pro 225	Tyr	Val	Arg	Gly	Ala 230	Leu	Asp	Tyr	Trp	Gly 235	Gln	Gly	Thr	Ser	Val 240
Thr	Val	Ser	Ser	Gly 245	Gly	Gly	Gly	Ser	Asp 250	Val	Gln	Leu	Val	Gln	Ser 255
Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala 265	Ser	Val	Lys	Val	Ser 270	Cys	Lys
Ala	Ser	Gly 275	Tyr	Thr	Phe	Thr	Arg	Tyr 280	Thr	Met	His	Trp 285	Val	Arg	Gln
Ala	Pro 290	Gly	Gln	Gly	Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Asn	Pro	Ser	Arg
Gly 305	Tyr	Thr	Asn	Tyr	Ala 310	Asp	Ser	Val	Lys	Gly 315	Arg	Phe	Thr	Ile	Thr 320
Thr	Asp	Lys	Ser	Thr	Ser	Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg 335
Ser	Glu	Asp	Thr	Ala	Thr	Tyr	Tyr	Cys 345	Ala	Arg	Tyr	Tyr	Asp	Asp	His 350
Tyr	Cys	Leu	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser 365

Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly
370 375 380

Ala Asp Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser
385 390 395 400

Pro. Gly Glu Arg Ala Thr Leu Thr Cys Arg Ala Ser Ser Ser Val Ser
405 410 415

Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp
420 425 430

Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser
435 440 445

Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu
450 455 460

Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro
465 470 475 480

Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
485 490

<210> 211

<211> 1476

<212> DNA

<213> artificial sequence

<220>

<223> CCR5xanti-CD3 VH7VL1

<400> 211

gacattatcc tgateccaatc tccaccttct ttggctgtgt ctctagggca gagggccacc 60

atctcctgca gaaccagcga aaatgttgac ggatacggca ttagttttat aaactggtac 120

caacagaagc caggacagcc acccaaactc ctcatctatg ctgcatccca ccaaggatcc 180

ggggtccttg ccagatttag tggcagtggg tctgggacag acttcagcct caacatccat 240

cctttggagg aggatgatac tgcaatgtat ttctgtcacc aaagtaagaa gggtccgtgg 300

acgttcggtg gaggcaccaa gctggaaatc aaaggtggtg gtggttctgg cggcggcggc 360

tccggtggtg gtggttctca gctggagcag tctggacctg aactgaagaa gcctggagag 420

acagtcacga tctcctgcaa ggcttctggg tataccttca cgaagtctgg aatgaactgg 480

gtgaagcagg ctccaggaaa gggtttaaag tggatgggct ggatacacac ctccactgga 540

gagccaacat attctgatga cttcaaggga cggtttgcct tctctttgga aacgtctgcc 600
agcactgcct atttgcggaat caacaacctc aaaaatgagg acatggctaa atacttctgt 660
gccagaggtg gtccttacgt aaggggtgct ttggactact ggggtcaagg aacctcagtc 720
accgtctcct ccggaggtgg tggatccgac gtccaactgg tgcagtcagg ggctgaagtg 780
aaaaaacctg gggcctcagt gaaggtgtcc tgcaaggctt ctggctacac ctttactagg 840
tacacgatgc actgggtaag gcaggcacct ggacagggtc tggaatggat tggatacatt 900
aatcctagcc gtgggttatac taattacaat cagaagttca aggaccgcgt cacaatcact 960
acagacaaat ccaccagcac agcctacatg gaactgagca gcctgcgttc tgaggacact 1020
gcagtctatt actgtgcaag atattatgat gatcattact gccttgacta ctggggccaa 1080
ggcaccacgg tcaccgtctc ctcaggcgaa ggtactagta ctgggttctgg tggaagtgga 1140
gggttcaggtg gagcagacga cattcagatg acccagtctc catctagcct gtctgcatct 1200
gtcggggacc gtgtcaccat cacctgcaga gccagtcaaa gtgtaagtta catgaactgg 1260
taccagcaga agccgggcaa ggcacccaaa agatggattt atgacacatc caaagtggct 1320
tctggagtcc ctgctcgctt cagtggcagt gggctctggga ccgactactc tctcacaatc 1380
aacagcttgg aggtgaaga tgctgccact tattactgcc aacagtggag tagtaacccg 1440
ctcacgttcg gtggcggggac caaggtggag atcaaa 1476

<210> 212
<211> 492
<212> PRT
<213> artificial sequence

<220>
<223> CCR5xanti-CD3 VH7VL1

<400> 212

Asp Ile Ile Leu Ile Gln Ser Pro Pro Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Arg Thr Ser Glu Asn Val Asp Gly Tyr
20 25 30

Gly Ile Ser Phe Ile Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Ala Ala Ser His Gln Gly Ser Gly Val Pro Ala
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Asn Ile His
65 70 75 80

Pro Leu Glu Glu Asp Asp Thr Ala Met Tyr Phe Cys His Gln Ser Lys
85 90 95

Lys Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Leu
115 120 125

Glu Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu Thr Val Thr Ile
130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Lys Phe Gly Met Asn Trp
145 150 155 160

Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met Gly Trp Ile His
165 170 175

Thr Ser Thr Gly Glu Pro Thr Tyr Ser Asp Asp Phe Lys Gly Arg Phe
180 185 190

Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr Leu Arg Ile Asn
195 200 205

Asn Leu Lys Asn Glu Asp Met Ala Lys Tyr Phe Cys Ala Arg Gly Gly
210 215 220

Pro Tyr Val Arg Gly Ala Leu Asp Tyr Trp Gly Gln Gly Thr Ser Val
225 230 235 240

Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Val Gln Leu Val Gln Ser
245 250 255

Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys
260 265 270

Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln
275 280 285

Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg
290 295 300

Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr
305 310 315 320

Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg
325 330 335

Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His
340 345 350

Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
355 360 365

Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly
370 375 380

Ala Asp Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
385 390 395 400

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser
405 410 415

Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp
420 425 430

Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser
435 440 445

Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu
450 455 460

Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro
465 470 475 480

Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
485 490

<210> 213

<211> 1476

<212> DNA

<213> artificial sequence

<220>

<223> CCR5xanti-CD3 VH7VL2

<400> 213

gacattatcc tgateccaatc tccaccttct ttggctgtgt ctctagggca gagggccacc

60

atctcctgca gaaccagcga aaatgttgac ggatacggca ttagttttat aaactggtac 120
caacagaagc caggacagcc acccaaactc ctcatctatg ctgcatccca ccaaggatcc 180
ggggtccctg ccagatttag tggcagtggg tctgggacag acttcagcct caacatccat 240
cctttggagg aggatgatac tgcaatgtat ttctgtcacc aaagtaagaa ggttccgtgg 300
acgttcggtg gaggcaccaa gctggaaatc aaaggtggtg gtggttctgg cggcggcggc 360
tccggtggtg gtggttctca gctggagcag tctggacctg aactgaagaa gcctggagag 420
acagtcacga tctcctgcaa ggcttctggg tataccttca cgaagtccgg aatgaactgg 480
gtgaagcagg ctccaggaaa gggtttaaag tggatgggct ggatacacac ctccactgga 540
gagccaacat attctgatga cttcaaggga cggtttgctt tctctttgga aacgtctgcc 600
agcactgcct atttgcggtat caacaacctc aaaaatgagg acatggctaa atacttctgt 660
gccagaggtg gtccttacgt aaggggtgct ttggactact ggggtcaagg aacctcagtc 720
accgtctcct ccggaggtgg tggatccgac gtccaactgg tgcagtcagg ggctgaagtg 780
aaaaaacctg gggcctcagt gaaggtgtcc tgcaaggctt ctggctacac ctttactagg 840
tacacgatgc actgggtaag gcaggcacct ggacagggtc tggaatggat tggatacatt 900
aatcctagcc gtggttatac taattacaat cagaagttca aggaccgcgt cacaatcact 960
acagacaaat ccaccagcac agcctacatg gaactgagca gcctgcgttc tgaggacact 1020
gcagtctatt actgtgcaag atattatgat gatcattact gccttgacta ctggggccaa 1080
ggcaccacgg tcaccgtctc ctcaggcgaa ggtactagta ctggttctgg tggaagtgga 1140
ggttcaggtg gagcagacga cattgtactg acccagtctc cagcaactct gtctctgtct 1200
ccagggggagc gtgccaccct gagctgcaga gccagtcaaa gtgtaagtta catgaactgg 1260
taccagcaga agccgggcaa ggcacccaaa agatggattt atgacacatc caaagtggct 1320
tctggagtcc ctgctcgctt cagtggcagt gggctctgga ccgactactc tctcacaatc 1380
aacagcttgg aggctgaaga tgctgccact tattactgcc aacagtggag tagtaaccgg 1440
ctcacgttcg gtggcggggac caaggtggag atcaaa 1476

<210> 214

<211> 492

<212> PRT

<213> artificial sequence

<220>

<223> CCR5xanti-CD3 VH7VL2

<400> 214

Asp Ile Ile Leu Ile Gln Ser Pro Pro Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Arg Thr Ser Glu Asn Val Asp Gly Tyr
20 25 30

Gly Ile Ser Phe Ile Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Ala Ala Ser His Gln Gly Ser Gly Val Pro Ala
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Asn Ile His
65 70 75 80

Pro Leu Glu Glu Asp Asp Thr Ala Met Tyr Phe Cys His Gln Ser Lys
85 90 95

Lys Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Leu
115 120 125

Glu Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu Thr Val Thr Ile
130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Lys Phe Gly Met Asn Trp
145 150 155 160

Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met Gly Trp Ile His
165 170 175

Thr Ser Thr Gly Glu Pro Thr Tyr Ser Asp Asp Phe Lys Gly Arg Phe
180 185 190

Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr Leu Arg Ile Asn
195 200 205

Asn Leu Lys Asn Glu Asp Met Ala Lys Tyr Phe Cys Ala Arg Gly Gly
210 215 220

Pro Tyr Val Arg Gly Ala Leu Asp Tyr Trp Gly Gln Gly Thr Ser Val
225 230 235 240

Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Val Gln Leu Val Gln Ser
245 250 255

Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys
260 265 270

Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln
275 280 285

Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg
290 295 300

Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr
305 310 315 320

Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg
325 330 335

Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His
340 345 350

Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
355 360 365

Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly
370 375 380

Ala Asp Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser
385 390 395 400

Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser
405 410 415

Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp
420 425 430

Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser
435 440 445

Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu
450 455 460

Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro

465

470

475

480

Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
485 490

<210> 215

<211> 1476

<212> DNA

<213> artificial sequence

<220>

<223> CCR5xanti-CD3 VH7VL3

<400> 215

gacattatcc tgateccaatc tccaccttct ttggctgtgt ctctagggca gagggccacc 60
atctcctgca gaaccagcga aaatgttgac ggatacggca ttagttttat aaactggtac 120
caacagaagc caggacagcc acccaaactc ctcatctatg ctgcatocca ccaaggatcc 180
ggggtccctg ccagatttag tggcagtggg tctgggacag acttcagcct caacatccat 240
cctttggagg aggatgatac tgcaatgtat ttctgtcacc aaagtaagaa ggttccgtgg 300
acgttcggtg gaggcaccaa gctggaaatc aaagggtggtg gtggttctgg cggcggcggc 360
tccggtggtg gtggttctca gctggagcag tctggacctg aactgaagaa gcctggagag 420
acagtcacga tctcctgcaa ggcttctggg tataccttca cgaagtctcg aatgaactgg 480
gtgaagcagg ctccaggaaa gggtttaaaag tggatgggct ggatacacac ctccactgga 540
gagccaacat attctgatga cttcaaggga cggtttgcct tctctttgga aacgtctgcc 600
agcactgcct atttgcgat caacaacctc aaaaatgagg acatggctaa atacttctgt 660
gccagaggtg gtccttacgt aaggggtgct ttggactact ggggtcaagg aacctcagtc 720
accgtctcct ccggaggtgg tggatccgac gtccaactgg tgcagtcagg ggctgaagtg 780
aaaaaacctg gggcctcagt gaagggtgcc tgcaaggctt ctggctacac ctttactagg 840
tacacgatgc actgggtaag gcaggcacct ggacagggtc tggaatggat tggatacatt 900
aatcctagcc gtggttatac taattacaat cagaagttca aggaccgcgt cacaatcact 960
acagacaaat ccaccagcac agcctacatg gaactgagca gcctgcgttc tgaggacact 1020
gcagtctatt actgtgcaag atattatgat gatcattact gccttgacta ctggggccaa 1080
ggcaccacgg tcaccgtctc ctcaaggcga ggtactagta ctggttctgg tggaagtgga 1140
ggttcaggtg gagcagacga cattgtactg acccagtctc cagcaactct gtctctgtct 1200
ccaggggagc gtgccaccct gacctgcaga gccagttcaa gtgtaagtta catgaactgg 1260
taccagcaga agccgggcaa ggcacccaaa agatggattt atgacacatc caaagtggct 1320

tctggagtc ctgctcgctt cagtggcagt gggctctggga ccgactactc tctcacaatc 1380
aacagcttgg aggtgaaga tgctgccact tattactgcc aacagtggag tagtaacccg 1440
ctcacgttcg gtggcgggac caaggtggag atcaaa 1476

<210> 216
<211> 492
<212> PRT
<213> artificial sequence

<220>
<223> CCR5xanti-CD3 VH7VL3

<400> 216

Asp Ile Ile Leu Ile Gln Ser Pro Pro Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Arg Thr Ser Glu Asn Val Asp Gly Tyr
20 25 30

Gly Ile Ser Phe Ile Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Ala Ala Ser His Gln Gly Ser Gly Val Pro Ala
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Asn Ile His
65 70 75 80

Pro Leu Glu Glu Asp Asp Thr Ala Met Tyr Phe Cys His Gln Ser Lys
85 90 95

Lys Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Leu
115 120 125

Glu Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu Thr Val Thr Ile
130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Lys Phe Gly Met Asn Trp
145 150 155 160

Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met Gly Trp Ile His

165

170

175

Thr Ser Thr Gly Glu Pro Thr Tyr Ser Asp Asp Phe Lys Gly Arg Phe
180 185 190

Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr Leu Arg Ile Asn
195 200 205

Asn Leu Lys Asn Glu Asp Met Ala Lys Tyr Phe Cys Ala Arg Gly Gly
210 215 220

Pro Tyr Val Arg Gly Ala Leu Asp Tyr Trp Gly Gln Gly Thr Ser Val
225 230 235 240

Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Val Gln Leu Val Gln Ser
245 250 255

Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys
260 265 270

Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln
275 280 285

Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg
290 295 300

Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr
305 310 315 320

Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg
325 330 335

Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His
340 345 350

Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
355 360 365

Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly
370 375 380

Ala Asp Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser
385 390 395 400

Pro Gly Glu Arg Ala Thr Leu Thr Cys Arg Ala Ser Ser Ser Val Ser
405 410 415

Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp
420 425 430

Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser
435 440 445

Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu
450 455 460

Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro
465 470 475 480

Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
485 490

<210> 217

<211> 1473

<212> DNA

<213> artificial sequence

<220>

<223> CD20xanti-CD3 VH5VL1

<400> 217

caaattgttc tctccagtc tccagcaatc ctttctgcat ctccagggga gaaggtcaca 60
atgacttgca gggccagctc aagtttaagt ttcatgcact ggtaccagca gaagccagga 120
tcctcccca aacctggat ttatgccaca tccaacctgg cttctggagt cctgctcgc 180
ttcagtggca gtgggtctgg gacctcttac tctctcaca tcagcagagt ggaggctgaa 240
gatgctgcca cttatttctg ccatcagtgg agtagtaacc cgctcacgtt cggtgctggg 300
acaaaggtgg aaataaaagg tgggtggtgg tctggcggcg gcggctccgg tgggtggtgg 360
tctcaggtgc aactgcggca gcctggggct gagctggtga agcctggggc ctcaagtgaag 420
atgtcctgca aggcttctgg ctacacattt accagttaca atatgcactg ggtaaagcag 480
acacctggac agggcctgga atggattgga gctatttata caggaaatgg tgatacttcc 540
tacaatcaga agttcaaagg caaggccaca ttgactgcag acaaatcctc cagcacagcc 600
tacatgcagc tcagcagtct gacatctgag gactctgcgg tctattactg tgcaagatcg 660
cactacggta gtaactacgt agactacttt gactactggg gccaaaggcac actagtcaca 720
gtctcgacag gaggtggtgg atccgacgtc caactggtgc agtcaggggc tgaagtgaag 780

```

aaacctgggg cctcagtga ggtgtcctgc aaggcttctg gctacacctt tactaggtac      840
acgatgcact gggtaaggca ggcacctgga cagggctctgg aatggattgg atacattaat      900
cctagccgtg gttatactaa ttacgcagac agcgtcaagg gccgcttcac aatcactaca      960
gacaaatcca ccagcacagc ctacatggaa ctgagcagcc tgcgttctga ggacactgca     1020
acctattact gtgcaagata ttatgatgat cattactgcc ttgactactg gggccaaggc     1080
accacgggtc ccgtctctc aggcgaaggc actagtactg gttctgggtg aagtggaggt     1140
tcaggtggag cagacgacat tcagatgacc cagtctccat ctacgctgtc tgcactctgtc     1200
ggggaccgtg tcaccatcac ctgcagagcc agtcaaagtg taagttacat gaactgggtac     1260
cagcagaagc cgggcaaggc acccaaaaga tggatttatg acacatccaa agtggcttct     1320
ggagtccttg ctcgcttcag tggcagtggg tctgggaccg actactctct cacaatcaac     1380
agcttggagg ctgaagatgc tgccacttat tactgccaac agtggagtag taacccgctc     1440
acgttcggtg gcgggaccaa ggtggagatc aaa                                1473

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<210> 218

<211> 491

<212> PRT

<213> artificial sequence

<220>

<223> CD20xanti-CD3 VH5VL1

<400> 218

```

Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly
1           5           10           15

```

```

Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Leu Ser Phe Met
          20           25           30

```

```

His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
          35           40           45

```

```

Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50           55           60

```

```

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu
65           70           75           80

```

```

Asp Ala Ala Thr Tyr Phe Cys His Gln Trp Ser Ser Asn Pro Leu Thr
          85           90           95

```

Phe Gly Ala Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly
100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Arg Gln Pro
115 120 125

Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys
130 135 140

Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn Met His Trp Val Lys Gln
145 150 155 160

Thr Pro Gly Gln Gly Leu Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn
165 170 175

Gly Asp Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr
180 185 190

Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr
195 200 205

Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Ser His Tyr Gly Ser
210 215 220

Asn Tyr Val Asp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
225 230 235 240

Val Ser Thr Gly Gly Gly Gly Ser Asp Val Gln Leu Val Gln Ser Gly
245 250 255

Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala
260 265 270

Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln Ala
275 280 285

Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly
290 295 300

Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Thr Thr
305 310 315 320

Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser
325 330 335

Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr
 340 345 350

Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly
 355 360 365

Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala
 370 375 380

Asp Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 385 390 395 400

Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Tyr
 405 410 415

Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile
 420 425 430

Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly
 435 440 445

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala
 450 455 460

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu
 465 470 475 480

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 485 490

<210> 219

<211> 1473

<212> DNA

<213> artificial sequence

<220>

<223> CD20xanti-CD3 VH5VL2

<400> 219

caaattgttc tctcccagtc tccagcaatc ctttctgcat ctccagggga gaaggtcaca 60

atgacttgca gggccagctc aagtttaagt ttcatgcact ggtaccagca gaagccagga 120

tcctccccca aaccctggat ttatgccaca tccaacctgg cttctggagt ccctgctcgc 180

ttcagtggca gtgggtctgg gacctcttac tctctcacia tcagcagagt ggaggctgaa 240

gatgctgcc cttatttctg ccatcagtg agtagtaacc cgctcacgtt cggtgctggg 300


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acaaaggtgg aaataaaagg tgggtggtggt tctggcggcg gcggctccgg tgggtggtggt 360
tctcaggtgc aactgcggca gcctggggct gagctggtga agcctggggc ctcaagtgaag 420
atgtcctgca aggcttctgg ctacacattt accagttaca atatgcactg ggtaaagcag 480
acacctggac agggcctgga atggattgga gctatttatc caggaaatgg tgatacttcc 540
tacaatcaga agttcaaagg caaggccaca ttgactgcag acaaatcctc cagcacagcc 600
tacatgcagc tcagcagtct gacatctgag gactctgcgg tctattactg tgcaagatcg 660
cactacggta gtaactacgt agactacttt gactactggg gccaaaggcac actagtcaca 720
gtctcgacag gaggtggtgg atccgacgtc caactggtgc agtcaggggc tgaagtgaaa 780
aaacctgggg cctcagtga ggtgtcctgc aaggcttctg gctacacctt tactaggtac 840
acgatgcact gggtaaggca ggcacctgga cagggtctgg aatggattgg atacattaat 900
cctagccgtg gttataactaa ttacgcagac agcgtcaagg gccgcttcac aatcactaca 960
gacaaatcca ccagcacagc ctacatggaa ctgagcagcc tgcgttctga ggacactgca 1020
acctattact gtgcaagata ttatgatgat cattactgcc ttgactactg gggccaaggc 1080
accacggcca ccgtctcctc aggcgaaggc actagtactg gttctggtgg aagtggaggt 1140
tcaggtggag cagacgacat tgtactgacc cagtctccag caactctgtc tctgtctcca 1200
ggggagcgtg ccacctgag ctgcagagcc agtcaaagtg taagttacat gaactggtac 1260
cagcagaagc cgggcaaggc acccaaaaga tggatttatg acacatccaa agtggcttct 1320
ggagtccctg ctgcgttcag tggcagtggg tctgggaccg actactctct cacaatcaac 1380
agcttgagg ctgaagatgc tgccacttat tactgccaac agtggagtag taaccgctc 1440
acgttcggtg gcgggaccaa ggtggagatc aaa 1473

```

<210> 220

<211> 491

<212> PRT

<213> artificial sequence

<220>

<223> CD20xanti-CD3 VH5VL2

<400> 220

```

Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly
1           5           10          15

```

```

Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Leu Ser Phe Met
20          25          30

```

His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
 35 40 45

Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Phe Cys His Gln Trp Ser Ser Asn Pro Leu Thr
 85 90 95

Phe Gly Ala Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly
 100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Arg Gln Pro
 115 120 125

Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys
 130 135 140

Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn Met His Trp Val Lys Gln
 145 150 155 160

Thr Pro Gly Gln Gly Leu Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn
 165 170 175

Gly Asp Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr
 180 185 190

Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr
 195 200 205

Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Ser His Tyr Gly Ser
 210 215 220

Asn Tyr Val Asp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
 225 230 235 240

Val Ser Thr Gly Gly Gly Gly Ser Asp Val Gln Leu Val Gln Ser Gly
 245 250 255

Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala
 260 265 270

Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln Ala
275 280 285

Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly
290 295 300

Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Thr Thr
305 310 315 320

Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser
325 330 335

Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr
340 345 350

Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly
355 360 365

Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala
370 375 380

Asp Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro
385 390 395 400

Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr
405 410 415

Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile
420 425 430

Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly
435 440 445

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala
450 455 460

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu
465 470 475 480

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
485 490

<211> 1473

<212> DNA

<213> artificial sequence

<220>

<223> CD20xanti-CD3 VH5VL3

<400> 221

caaattgttc tctcccagtc tccagcaatc ctttctgcat ctccagggga gaaggtcaca	60
atgacttgca gggccagctc aagttttaagt ttcattgcact ggtaccagca gaagccagga	120
tctccccca aaccctggat ttatgccaca tccaacctgg cttctggagt ccttgctcgc	180
ttcagtggca gtgggtctgg gacctcttac tctctcacia tcagcagagt ggaggctgaa	240
gatgctgcca cttatttctg ccatcagtgg agtagtaacc cgctcacgtt cggtgctggg	300
acaaagggtg aaataaaagg tgggtgggtg tctggcgggc gcggctccgg tgggtgggtg	360
tctcaggtgc aactgcggca gcctggggct gagctgggtg agcctggggc ctcagtgaag	420
atgtcctgca aggcttctgg ctacacattt accagttaca atatgcactg ggtaaagcag	480
acacctggac agggcctgga atggattgga gctattttatc caggaaatgg tgatacttcc	540
tacaatcaga agttcaaagg caaggccaca ttgactgcag acaaatectc cagcacagcc	600
tacatgcagc tcagcagtct gacatctgag gactctgcgg tctattactg tgcaagatcg	660
cactacggta gtaactacgt agactacttt gactactggg gccaaaggcac actagtcaca	720
gtctcgacag gaggtgggtg atccgacgtc caactgggtg agtcaggggc tgaagtgaaa	780
aaacctgggg cctcagtga ggtgtcctgc aaggcttctg gctacacctt tactaggtac	840
acgatgcact gggtaaggca ggcacctgga cagggtctgg aatggattgg atacattaat	900
cctagccgtg gttataactaa ttacgcagac agcgtcaagg gccgcttcac aatcactaca	960
gacaaatcca ccagcacagc ctacatggaa ctgagcagcc tgcgttctga ggacactgca	1020
acctattact gtgcaagata ttatgatgat cattactgcc ttgactactg gggccaaggc	1080
accacgggtc ccgtctcctc aggcgaaggc actagtactg gttctgggtg aagtggaggt	1140
tcagggtggag cagacgacat tgtactgacc cagtctccag caactctgtc tctgtctcca	1200
ggggagcgtg ccacctgac ctgcagagcc agttcaagtg taagttacat gaactggtac	1260
cagcagaagc cgggcaaggc acccaaaaga tggatttatg acacatccaa agtggcttct	1320
ggagtccttg ctgcgttcag tggcagtggg tctgggaccg actactctct cacaatcaac	1380
agcttggagg ctgaagatgc tgccacttat tactgccaac agtggagtag taaccgctc	1440
acgttcggtg gcgggaccaa ggtggagatc aaa	1473

<210> 222
 <211> 491
 <212> PRT
 <213> artificial sequence

<220>
 <223> CD20xanti-CD3 VH5VL3

<400> 222

Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly
 1 5 10 15

Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Leu Ser Phe Met
 20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
 35 40 45

Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Phe Cys His Gln Trp Ser Ser Asn Pro Leu Thr
 85 90 95

Phe Gly Ala Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly
 100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Arg Gln Pro
 115 120 125

Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys
 130 135 140

Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn Met His Trp Val Lys Gln
 145 150 155 160

Thr Pro Gly Gln Gly Leu Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn
 165 170 175

Gly Asp Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr
 180 185 190

Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr

195

200

205

Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Ser	His	Tyr	Gly	Ser
210						215					220				
Asn	Tyr	Val	Asp	Tyr	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr
225					230					235					240
Val	Ser	Thr	Gly	Gly	Gly	Gly	Ser	Asp	Val	Gln	Leu	Val	Gln	Ser	Gly
				245					250					255	
Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala
			260					265					270		
Ser	Gly	Tyr	Thr	Phe	Thr	Arg	Tyr	Thr	Met	His	Trp	Val	Arg	Gln	Ala
		275					280					285			
Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Asn	Pro	Ser	Arg	Gly
	290					295					300				
Tyr	Thr	Asn	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Thr	Thr
305					310					315					320
Asp	Lys	Ser	Thr	Ser	Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser
				325					330					335	
Glu	Asp	Thr	Ala	Thr	Tyr	Tyr	Cys	Ala	Arg	Tyr	Tyr	Asp	Asp	His	Tyr
			340					345					350		
Cys	Leu	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly
		355					360					365			
Glu	Gly	Thr	Ser	Thr	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Ala
	370					375					380				
Asp	Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Leu	Ser	Pro
385					390					395					400
Gly	Glu	Arg	Ala	Thr	Leu	Thr	Cys	Arg	Ala	Ser	Ser	Ser	Val	Ser	Tyr
				405					410					415	
Met	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Arg	Trp	Ile
			420					425					430		

Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly
 435 440 445

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala
 450 455 460

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu
 465 470 475 480

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 485 490

<210> 223
 <211> 1473
 <212> DNA
 <213> artificial sequence

<220>
 <223> CD20xanti-CD3 VH7VL1

<400> 223
 caaatgttgc tctcccagtc tccagcaatc ctttctgcat ctccagggga gaaggtcaca 60
 atgacttgca gggccagctc aagtttaagt ttcatgcact ggtaccagca gaagccagga 120
 tcctccccca aaccctggat ttatgccaca tccaacctgg cttctggagt cctgctcgc 180
 ttcagtggca gtgggtctgg gacctcttac tctctcacia tcagcagagt ggaggctgaa 240
 gatgctgcca cttatttctg ccatcagtggt agtagtaacc cgctcacgtt cgggtgctggg 300
 acaaaggtgg aaataaaagg tgggtggtggt tctggcggcg gcggctccgg tgggtggtggt 360
 tctcaggtgc aactgcggca gcctggggct gagctggtga agcctggggc ctcaagtgaag 420
 atgtcctgca aggcttctgg ctacacattt accagttaca atatgcactg ggtaaagcag 480
 acacctggac agggcctgga atggattgga gctatttata caggaaatgg tgatacttcc 540
 tacaatcaga agttcaaagg caaggccaca ttgactgcag acaaatcctc cagcacagcc 600
 tacatgcagc tcagcagtct gacatctgag gactctgcgg tctattactg tgcaagatcg 660
 cactacggta gtaactacgt agactacttt gactactggg gccaaggcac actagtcaca 720
 gtctcgacag gaggtggtgg atccgacgtc caactggtgc agtcaggggc tgaagtgaaa 780
 aaacctgggg cctcagtga ggtgtcctgc aaggcttctg gctacacctt tactaggtac 840
 acgatgcact gggtaaggca ggcacctgga cagggtctgg aatggattgg atacattaat 900
 cctagccgtg gttataactaa ttacaatcag aagttcaagg accgcgtcac aatcactaca 960
 gacaaatcca ccagcacagc ctacatggaa ctgagcagcc tgcgttctga ggacactgca 1020

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gtctattact gtgcaagata ttatgatgat cattactgcc ttgactactg gggccaaggc 1080
accacgggtca ccgtctcctc aggcgaaggt actagtactg gttctgggtg aagtggaggt 1140
tcaggtggag cagacgacat tcagatgacc cagtctccat ctagcctgtc tgcattctgtc 1200
ggggaccgtg tcaccatcac ctgcagagcc agtcaaagtg taagttacat gaactgggtac 1260
cagcagaagc cgggcaaggc acccaaaaga tggatttatg acacatccaa agtgggttct 1320
ggagtccttg ctgccttcag tggcagtggg tctgggaccg actactctct cacaatcaac 1380
agcttggagg ctgaagatgc tgccacttat tactgccaac agtggagtag taacccgctc 1440
acgttcggtg gcgggaccaa ggtggagatc aaa 1473

```

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<210> 224
<211> 491
<212> PRT
<213> artificial sequence

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<220>
<223> CD20xanti-CD3 VH7VL1

```

```

<400> 224

```

```

Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly
1           5           10           15

```

```

Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Leu Ser Phe Met
20           25           30

```

```

His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
35           40           45

```

```

Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50           55           60

```

```

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu
65           70           75           80

```

```

Asp Ala Ala Thr Tyr Phe Cys His Gln Trp Ser Ser Asn Pro Leu Thr
85           90           95

```

```

Phe Gly Ala Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly
100          105          110

```

```

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Arg Gln Pro
115          120          125

```


Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys
130 135 140

Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn Met His Trp Val Lys Gln
145 150 155 160

Thr Pro Gly Gln Gly Leu Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn
165 170 175

Gly Asp Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr
180 185 190

Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr
195 200 205

Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Ser His Tyr Gly Ser
210 215 220

Asn Tyr Val Asp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
225 230 235 240

Val Ser Thr Gly Gly Gly Gly Ser Asp Val Gln Leu Val Gln Ser Gly
245 250 255

Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala
260 265 270

Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln Ala
275 280 285

Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly
290 295 300

Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Thr
305 310 315 320

Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser
325 330 335

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr
340 345 350

Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly
355 360 365

Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala
370 375 380

Asp Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
385 390 395 400

Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Tyr
405 410 415

Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile
420 425 430

Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly
435 440 445

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala
450 455 460

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu
465 470 475 480

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
485 490

<210> 225
<211> 1473
<212> DNA
<213> artificial sequence

<220>
<223> CD20xanti-CD3 VH7VL2

<400> 225
caaattgttc tctcccagtc tccagcaatc ctttctgcat ctccagggga gaaggtcaca 60
atgacttgca gggccagctc aagtttaagt ttcattgact ggtaccagca gaagccagga 120
tcctcccca aaccctggat ttatgccaca tccaacctgg cttctggagt ccctgctcgc 180
ttcagtggca gtgggtctgg gacctttac tctctcacia tcagcagagt ggaggctgaa 240
gatgctgcca cttatttctg ccatcagtgg agtagtaacc cgctcacgtt cggtgctggg 300
acaaagggtg aaataaaagg tgggtggtgg tctggcgggc gcggctccgg tgggtggtgg 360
tctcaggtgc aactgcggca gcctggggct gagctggtga agcctggggc ctcagtgaag 420
atgtcctgca aggcttctgg ctacacattt accagttaca atatgcactg ggtaaagcag 480
acacctggac agggcctgga atggattgga gctatttatc caggaaatgg tgatacttcc 540

tacaatcaga agttcaaagg caaggccaca ttgactgcag acaaatcctc cagcacagcc 600
 tacatgcagc tcagcagtct gacatctgag gactctgcgg tctattactg tgcaagatcg 660
 cactacggta gtaactacgt agactacttt gactactggg gccaaaggcac actagtcaca 720
 gtctcgacag gaggtggtgg atccgacgtc caactggtgc agtcaggggc tgaagtgaaa 780
 aaacctgggg cctcagtga ggtgtcctgc aaggcttctg gctacacctt tactaggtac 840
 acgatgcact gggtaaggca ggcacctgga cagggtctgg aatggattgg atacattaat 900
 cctagccgtg gttataactaa ttacaatcag aagttcaagg accgcgtcac aatcactaca 960
 gacaaatcca ccagcacagc ctacatggaa ctgagcagcc tgcgttctga ggacactgca 1020
 gtctattact gtgcaagata ttatgatgat cattactgcc ttgactactg gggccaaggc 1080
 accacggta cagtctctc aggcgaagg actagtactg gttctggtg aagtggaggt 1140
 tcagggtggag cagacgacat tgtactgacc cagtctccag caactctgtc tctgtctcca 1200
 ggggagcgtg ccaccctgag ctgcagagcc agtcaaagtg taagttacat gaactggtac 1260
 cagcagaagc cgggcaaggc acccaaaaga tggatttatg acacatccaa agtggcttct 1320
 ggagtcctg ctgccttcag tggcagtggg tctgggaccg actactctct cacaatcaac 1380
 agcttgagg ctgaagatgc tgccacttat tactgccaac agtggagtag taaccgctc 1440
 acgttcggtg gcgggaccaa ggtggagatc aaa 1473

<210> 226
 <211> 491
 <212> PRT
 <213> artificial sequence

<220>
 <223> CD20xanti-CD3 VH7VL2

<400> 226

Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly
 1 5 10 15

Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Leu Ser Phe Met
 20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
 35 40 45

Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Phe Cys His Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

Phe Gly Ala Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly
100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Arg Gln Pro
115 120 125

Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys
130 135 140

Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn Met His Trp Val Lys Gln
145 150 155 160

Thr Pro Gly Gln Gly Leu Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn
165 170 175

Gly Asp Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr
180 185 190

Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr
195 200 205

Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Ser His Tyr Gly Ser
210 215 220

Asn Tyr Val Asp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
225 230 235 240

Val Ser Thr Gly Gly Gly Gly Ser Asp Val Gln Leu Val Gln Ser Gly
245 250 255

Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala
260 265 270

Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln Ala
275 280 285

Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly
290 295 300

Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Thr
 305 310 315 320

Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser
 325 330 335

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr
 340 345 350

Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly
 355 360 365

Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala
 370 375 380

Asp Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro
 385 390 395 400

Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr
 405 410 415

Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile
 420 425 430

Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly
 435 440 445

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala
 450 455 460

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu
 465 470 475 480

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 485 490

<210> 227
 <211> 1473
 <212> DNA
 <213> artificial sequence

<220>
 <223> CD20xanti-CD3 VH7VL3

<400> 227

caaattgttc tctcccagtc tccagcaatc ctttctgcat ctccagggga gaaggtcaca 60
atgacttgca gggccagctc aagtttaagt ttcatgcact ggtaccagca gaagccagga 120
tcctcccca aaccctggat ttatgccaca tccaacctgg cttctggagt ccctgctcgc 180
ttcagtggca gtgggtctgg gacctcttac tctctcacia tcagcagagt ggaggctgaa 240
gatgctgcca cttatttctg ccatcagtgg agtagtaacc cgctcacgtt cggtgctggg 300
acaaagggtg aaataaaagg tgggtgggtg tctggcggcg gcggctccgg tgggtgggtg 360
tctcagggtg aactgcggca gcctggggct gagctgggtg agcctggggc ctcagtgaag 420
atgtcctgca aggcttctgg ctacacattt accagttaca atatgcactg ggtaaagcag 480
acacctggac agggcctgga atggattgga gctatttata caggaaatgg tgatacttcc 540
tacaatcaga agttcaaagg caaggccaca ttgactgcag acaaatcctc cagcacagcc 600
tacatgcagc tcagcagtct gacatctgag gactctgcgg tctattactg tgcaagatcg 660
cactacggta gtaactacgt agactacttt gactactggg gccaaaggcac actagtcaca 720
gtctcgacag gaggtgggtg atccgacgtc caactgggtg agtcaggggc tgaagtgaag 780
aaacctgggg cctcagtga ggtgtcctgc aaggcttctg gctacacctt tactaggtac 840
acgatgcact gggtaaggca ggcacctgga caggggtctg aatggattgg atacattaat 900
cctagccgtg gttataactaa ttacaatcag aagttcaagg accgcgtcac aatcactaca 960
gacaaatcca ccagcacagc ctacatggaa ctgagcagcc tgcgttctga ggacactgca 1020
gtctattact gtgcaagata ttatgatgat cattactgcc ttgactactg gggccaaggc 1080
accacggtea ccgtctctc aggccaagg actagtactg gttctgggtg aagtggagg 1140
tcagggtggag cagacgacat tgtactgacc cagtctccag caactctgtc tctgtctcca 1200
ggggagcgtg ccacctgac ctgcagagcc agttcaagtg taagttacat gaactgggtac 1260
cagcagaagc cgggcaaggc acccaaaaga tggatttatg acacatccaa agtggcttct 1320
ggagtccctg ctgcgttcag tggcagtggg tctgggaccg actactctct cacaatcaac 1380
agcttgagg ctgaagatgc tgccacttat tactgccaac agtggagtag taaccgcgtc 1440
acgttcggtg gcgggaccaa ggtggagatc aaa 1473

<210> 228

<211> 491

<212> PRT

<213> artificial sequence

<220>

<223> CD20xanti-CD3 VH7VL3

<400> 228

Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly
 1 5 10 15

Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Leu Ser Phe Met
 20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
 35 40 45

Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Phe Cys His Gln Trp Ser Ser Asn Pro Leu Thr
 85 90 95

Phe Gly Ala Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly
 100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Arg Gln Pro
 115 120 125

Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys
 130 135 140

Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn Met His Trp Val Lys Gln
 145 150 155 160

Thr Pro Gly Gln Gly Leu Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn
 165 170 175

Gly Asp Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr
 180 185 190

Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr
 195 200 205

Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Ser His Tyr Gly Ser
 210 215 220

Asn Tyr Val Asp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr

225		230		235		240
Val Ser Thr Gly Gly Gly Gly Ser Asp Val Gln Leu Val Gln Ser Gly						
		245		250		255
Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala						
		260		265		270
Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln Ala						
		275		280		285
Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly						
		290		295		300
Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Thr						
		305		310		315
						320
Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser						
		325		330		335
Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr						
		340		345		350
Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly						
		355		360		365
Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala						
		370		375		380
Asp Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro						
		385		390		395
						400
Gly Glu Arg Ala Thr Leu Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr						
		405		410		415
Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile						
		420		425		430
Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly						
		435		440		445
Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala						
		450		455		460

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu
465 470 475 480

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
485 490

<210> 229
<211> 25
<212> PRT
<213> artificial sequence

<220>
<223> non-deimmunized anti-CD3 Framework 1

<400> 229

Asp Ile Lys Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Thr Ser
20 25

<210> 230
<211> 15
<212> PRT
<213> artificial sequence

<220>
<223> non-deimmunized anti-CD3 Framework 2

<400> 230

Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr
1 5 10 15

<210> 231
<211> 32
<212> PRT
<213> artificial sequence

<220>
<223> non-deimmunized anti-CD3 Framework 3

<400> 231

Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln
1 5 10 15

Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 232

<211> 11
<212> PRT
<213> artificial sequence

<220>
<223> non-deimmunized anti-CD3 Framework 4

<400> 232

Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
1 5 10

<210> 233
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> Sequence motif

<400> 233

Ala Ser Gly Tyr Thr Phe
1 5

<210> 234
<211> 4
<212> PRT
<213> artificial sequence

<220>
<223> Sequence motif

<400> 234

Met Glu Leu Ser
1

<210> 235
<211> 5
<212> PRT
<213> artificial sequence

<220>
<223> Sequence motif

<400> 235

Ile Thr Thr Asp Lys
1 5

<210> 236
<211> 1488
<212> DNA
<213> artificial sequence

<220>

<223> 5-10xVH5VL1 LHHL

<400> 236

gagctcgtga tgacacagtc tccatcctcc ctgactgtga cagcaggaga gaaggtcact	60
atgagctgca agtccagtca gagtctgtta aacagtggaa atcaaaagaa ctacttgacc	120
tggtaccagc agaaaccagg gcagcctcct aaactgttga tctactgggc atccactagg	180
gaatctgggg tccctgatcg cttcacaggc agtggatctg gaacagatth cactctcacc	240
atcagcagtg tgcaggctga agacctggca gtttattact gtcagaatga ttatagttat	300
ccgctcacgt tcggtgctgg gaccaagctt gagatcaaag gtggtggtgg ttctggcggc	360
ggcggctccg gtggtggtgg ttctgaggtg cagctgctcg agcagtctgg agctgagctg	420
gtaaggcctg ggacttcagt gaagatatcc tgcaaggctt ctggatacgc cttcactaac	480
tactggctag gttgggtaaa gcagaggcct ggacatggac ttgagtggat tggagatatt	540
ttccctggaa gtggtaatat ccactacaat gagaagttca agggcaaagc cacactgact	600
gcagacaaat cttcgagcac agcctatatg cagctcagta gcctgacatt tgaggactct	660
gctgtctatt tctgtgcaag actgaggaac tgggacgagc ctatggacta ctggggccaa	720
gggaccacgg tcaccgtctc ctccggaggt ggtggatccg acgtccaact ggtgcagtca	780
ggggctgaag tgaaaaaacc tggggcctca gtgaagggtg cctgcaaggc ttctggctac	840
acctttacta ggtacacgat gcactgggta aggcaggcac ctggacaggg tctggaatgg	900
attggataca ttaatcctag ccgtgggttat actaattacg cagacagcgt caagggccgc	960
ttcacaatca ctacagacaa atccaccagc acagcctaca tggaactgag cagcctgcgt	1020
tctgaggaca ctgcaacctt ttactgtgca agatattatg atgatcatta ctgccttgac	1080
tactggggcc aaggcaccac ggtcacctgc tccctcaggcg aaggtagtag tactggttct	1140
ggtggaagtg gaggttcagg tggagcagac gacattcaga tgaccagtc tccatctagc	1200
ctgtctgcat ctgtcgggga ccgtgtcacc atcacctgca gagccagtca aagtgttaagt	1260
tacatgaact ggtaccagca gaagccgggc aaggcaccca aaagatggat ttatgacaca	1320
tccaaagtgg cttctggagt ccctgctcgc ttcagtggca gtgggtctgg gaccgactac	1380
tctctcacia tcaacagctt ggaggctgaa gatgctgcca cttattactg ccaacagtgg	1440
agtagtaacc cgctcacgtt cgggtggcggg accaaggtgg agatcaaa	1488

<210> 237

<211> 496

<212> PRT

<213> artificial sequence

<220>

<223> 5-10xVH5VL1 LHHL

<400> 237

Glu Leu Val Met Thr Gln Ser Pro Ser Ser Leu Thr Val Thr Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Asp Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile
100 105 110

Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
130 135 140

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
145 150 155 160

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
165 170 175

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
180 185 190

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
195 200 205

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
210 215 220

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
225 230 235 240

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Val Gln
245 250 255

Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys
260 265 270

Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His
275 280 285

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile
290 295 300

Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg
305 310 315 320

Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu
325 330 335

Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr
340 345 350

Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val
355 360 365

Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser Gly
370 375 380

Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
385 390 395 400

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
405 410 415

Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
420 425 430

Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro
435 440 445

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
450 455 460

Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
465 470 475 480

Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
485 490 495

<210> 238

<211> 1491

<212> DNA

<213> artificial sequence

<220>

<223> 5-10xVH5VL1 HLHL

<400> 238

gaggtgcagc tgctcgagca gtctggagct gagctggtaa ggcctgggac ttcagtgaag 60
atatacctgca aggcttctgg atacgccttc actaactact ggctagggttg ggtaaagcag 120
aggcctggac atggacttga gtggattgga gatattttcc ctggaagtgg taatatccac 180
tacaatgaga agttcaaggg caaagccaca ctgactgcag acaaactctc gagcacagcc 240
tatatgcagc tcagtagcct gacatttgag gactctgctg tctatttctg tgcaagactg 300
aggaactggg acgagcctat ggactactgg ggccaaggga ccacggtcac cgtctcctca 360
ggtgggtggtg gttctggcgg cggcggctcc ggtgggtggtg gttctgagct cgtgatgaca 420
cagtctccat cctccctgac tgtgacagca ggagagaagg tcactatgag ctgcaagtcc 480
agtcagagtc tgtaaacag tggaaatcaa aagaactact tgacctggtg ccagcagaaa 540
ccagggcagc ctctaaact gttgatctac tgggcatcca ctagggaatc tggggtcctc 600
gatcgcttca caggcagtgg atctggaaca gatttcactc tcaccatcag cagtgtgcag 660
gctgaagacc tggcagttta ttactgtcag aatgattata gttatccgct cacgttcggt 720
gctgggacca agcttgagat caaatccgga ggtgggtggat ccgacgtcca actgggtgcag 780
tcaggggctg aagtgaaaaa acctggggcc tcagtgaagg tgcctgcaa ggcttctggc 840
tacaccttta ctaggtacac gatgcactgg gtaaggcagg cacctggaca gggctctggaa 900
tggtattgat acattaatcc tagccgtggt tataactaatt acgcagacag cgtcaagggc 960
cgcttcacaa tcactacaga caaatccacc agcacagcct acatggaact gagcagcctg 1020
cgcttctgagg aactgcaac ctattactgt gcaagatatt atgatgatca ttactgcctt 1080
gactactggg gccaaaggcac cacggtcacc gtctcctcag gcgaagggtac tagtactggt 1140

tctggtggaa gtggagggttc aggtggagca gacgacattc agatgaccca gtctccatct 1200
 agcctgtctg catctgtcgg ggaccgtgtc accatcacct gcagagccag tcaaagtgtg 1260
 agttacatga actggtacca gcagaagccg ggcaaggcac ccaaaagatg gatttatgac 1320
 acatccaaag tggcttctgg agtccttgct cgcttcagtg gcagtgggtc tgggaccgac 1380
 tactctctca caatcaacag cttggagggt gaagatgctg ccacttatta ctgccaacag 1440
 tggagtagta acccgctcac gttcgggtggc gggaccaagg tggagatcaa a 1491

<210> 239

<211> 497

<212> PRT

<213> artificial sequence

<220>

<223> 5-10xVH5VL1 HLHL

<400> 239

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
 1 5 10 15

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
 20 25 30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
 35 40 45

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
 50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
 65 70 75 80

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
 85 90 95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser
 130 135 140

Ser Leu Thr Val Thr Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser
 145 150 155 160

Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu Thr Trp
 165 170 175

Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala
 180 185 190

Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser
 195 200 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu
 210 215 220

Ala Val Tyr Tyr Cys Gln Asn Asp Tyr Ser Tyr Pro Leu Thr Phe Gly
 225 230 235 240

Ala Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Asp Val
 245 250 255

Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val
 260 265 270

Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met
 275 280 285

His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr
 290 295 300

Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly
 305 310 315 320

Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu
 325 330 335

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg
 340 345 350

Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr
 355 360 365

Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser
 370 375 380

Gly Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser Pro Ser
385 390 395 400

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
405 410 415

Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys
420 425 430

Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val
435 440 445

Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr
450 455 460

Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
465 470 475 480

Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
485 490 495

Lys

<210> 240
<211> 1488
<212> DNA
<213> artificial sequence

<220>
<223> 5-10xVL1VH5 LHLH

<400> 240
gagctcgtga tgacacagtc tccatcctcc ctgactgtga cagcaggaga gaaggtcact 60
atgagctgca agtccagtca gagtctgtta aacagtggaa atcaaaagaa ctacttgacc 120
tggtaccagc agaaaccagg gcagcctcct aaactgttga tctactgggc atccactagg 180
gaatctgggg tccctgatcg cttcacaggc agtggatctg gaacagattt cactctcacc 240
atcagcagtg tgcaggctga agacctggca gtttattact gtcagaatga ttatagttat 300
ccgctcacgt tcggtgctgg gaccaagctt gagatcaaag gtggtggtgg ttctggcggc 360
ggcggctccg gtggtggtgg ttctgaggtg cagctgctcg agcagtctgg agctgagctg 420
gtaaggcctg ggacttcagt gaagatatcc tgcaaggctt ctggatacgc cttcactaac 480

tactggctag gttgggtaaa gcagaggcct ggacatggac ttgagtggat tggagatatt 540
 ttccctggaa gtggtaatat ccactacaat gagaagttca agggcaaagc cacactgact 600
 gcagacaaat cttcgagcac agcctatatg cagctcagta gcctgacatt tgaggactct 660
 gctgtctatt tctgtgcaag actgaggaac tgggacgagc ctatggacta ctggggccaa 720
 gggaccacgg tcacogtctc ctccggaggt ggtggatccg acattcagat gaccagctct 780
 ccatctagcc tgtctgcatc tgctggggac cgtgtcacca tcacctgcag agccagtcaa 840
 agtgtaagtt acatgaactg gtaccagcag aagccgggca aggcacccaa aagatggatt 900
 tatgacacat ccaaagtggc ttctggagtc cctgctcgct tcagtggcag tgggtctggg 960
 accgactact ctctcacaat caacagcttg gaggctgaag atgctgccac ttattactgc 1020
 caacagtgga gtagtaacct gctcacgttc ggtggcgga ccaaggtgga gatcaaagge 1080
 gaaggtacta gtactgggtc tgggtggaagt ggaggttcag gtggagcaga cgacgtccaa 1140
 ctggtgcagt caggggctga agtgaaaaaa cctggggcct cagtgaaggt gtcctgcaag 1200
 gcttctggct acacctttac taggtacacg atgcactggg taaggcagge acctggacag 1260
 ggtctggaat ggattggata cattaatcct agccgtgggt atactaatta cgcagacagc 1320
 gtcaagggcc gcttcacaat cactacagac aaatccacca gcacagccta catggaactg 1380
 agcagcctgc gttctgagga cactgcaacc tattactgtg caagatatta tgatgatcat 1440
 tactgccttg actactgggg ccaaggcacc acggtcaccg tctcctca 1488

<210> 241
 <211> 496
 <212> PRT
 <213> artificial sequence

<220>
 <223> 5-10xVL1VH5 LHLH

<400> 241

Glu Leu Val Met Thr Gln Ser Pro Ser Ser Leu Thr Val Thr Ala Gly
 1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
 20 25 30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80
 Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Asn
 85 90 95
 Asp Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile
 100 105 110
 Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 115 120 125
 Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
 130 135 140
 Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
 145 150 155 160
 Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
 165 170 175
 Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
 180 185 190
 Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
 195 200 205
 Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
 210 215 220
 Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
 225 230 235 240
 Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Gln
 245 250 255
 Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
 260 265 270
 Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr
 275 280 285
 Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser

290

295

300

Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
305 310 315 320

Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala
325 330 335

Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly
340 345 350

Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr Gly Ser Gly
355 360 365

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu Val Gln Ser
370 375 380

Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys
385 390 395 400

Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln
405 410 415

Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg
420 425 430

Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Thr
435 440 445

Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg
450 455 460

Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His
465 470 475 480

Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
485 490 495

<210> 242

<211> 1491

<212> DNA

<213> artificial sequence

<220>

<223> 5-10xVL1VH5 HLLH

<400> 242

gaggtgcagc tgctcgagca gtctggagct gagctggtaa ggcctgggac ttcagtgaag	60
atatcctgca aggttcttgg atacgccttc actaactact ggctaggttg ggtaaagcag	120
aggcctggac atggacttga gtggattgga gatattttcc ctggaagtgg taatatccac	180
tacaatgaga agttcaaggg caaagccaca ctgactgcag acaaatcttc gagcacagcc	240
tatatgcagc tcagtagcct gacatttgag gactctgctg tctattttctg tgcaagactg	300
aggaactggg acgagcctat ggactactgg ggccaaggga ccacggtcac cgtctcctca	360
ggtggtggtg gttctggcgg cggcggctcc ggtggtggtg gttctgagct cgtgatgaca	420
cagtctccat cctccctgac tgtgacagca ggagagaagg tcactatgag ctgcaagtcc	480
agtcagagtc tgttaaacag tggaaatcaa aagaactact tgacctggta ccagcagaaa	540
ccagggcagc ctccctaaact gttgatctac tgggcatcca ctagggaatc tggggtcctc	600
gatcgcttca caggcagtgg atctggaaca gatttcactc tcaccatcag cagtgtgcag	660
gctgaagacc tggcagttta ttactgtcag aatgattata gttatccgct cacgttcggt	720
gctgggacca agcttgagat caaatccgga ggtggtggat ccgacattca gatgaccag	780
tctccatcta gcctgtctgc atctgtcggg gaccgtgtca ccatcacctg cagagccagt	840
caaagtgtaa gttacatgaa ctggtaccag cagaagccgg gcaaggcacc caaaagatgg	900
atttatgaca catccaaagt ggcttctgga gtccctgctc gcttcagtgg cagtgggtct	960
gggaecgact actctctcac aatcaacagc ttggaggctg aagatgctgc cacttattac	1020
tgccaacagt ggagtagtaa cccgctcacg ttcggtggcg ggaccaaggt ggagatcaaa	1080
ggcgaaggta ctagtactgg ttctggtgga agtggagggt cagggtggagc agacgacgtc	1140
caactggtgc agtcaggggc tgaagtgaaa aaacctgggg cctcagtga ggtgtcctgc	1200
aaggcttctg gctacacctt tactaggtac acgatgcact gggtaaggca ggcacctgga	1260
cagggtctgg aatggattgg atacattaat cctagccgtg gttatactaa ttacgcagac	1320
agcgtcaagg gccgcttcac aatcactaca gacaaatcca ccagcacagc ctacatggaa	1380
ctgagcagcc tgcgttctga ggacactgca acctattact gtgcaagata ttatgatgat	1440
cattactgcc ttgactactg gggccaaggc accacggtca ccgtctcctc a	1491

<210> 243

<211> 497

<212> PRT

<213> artificial sequence

<220>

<223> 5-10xVL1VH5 HLLH

<400> 243

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
1 5 10 15

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
20 25 30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
35 40 45

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
65 70 75 80

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
85 90 95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser
130 135 140

Ser Leu Thr Val Thr Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser
145 150 155 160

Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu Thr Trp
165 170 175

Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala
180 185 190

Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser
195 200 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu
210 215 220

Ala Val Tyr Tyr Cys Gln Asn Asp Tyr Ser Tyr Pro Leu Thr Phe Gly
225 230 235 240

Ala Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Asp Ile
245 250 255

Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
260 265 270

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp
275 280 285

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr
290 295 300

Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser
305 310 315 320

Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala
325 330 335

Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly
340 345 350

Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr Gly Ser
355 360 365

Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu Val Gln
370 375 380

Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys
385 390 395 400

Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg
405 410 415

Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser
420 425 430

Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile
435 440 445

Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu
450 455 460

Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp
465 470 475 480

His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser
485 490 495

Ser

<210> 244
<211> 1491
<212> DNA
<213> artificial sequence

<220>
<223> 5-10xVH5VL2 HLHL

<400> 244
gaggtgcagc tgctcgagca gtctggagct gagctggtaa ggcctgggac ttcagtgaag 60
atatcctgca aggcttctgg atacgccttc actaactact ggctaggttg ggtaaagcag 120
aggcctggac atggacttga gtggattgga gatattttcc ctggaagtgg taatatccac 180
tacaatgaga agttcaaggg caaagccaca ctgactgcag acaaattctc gagcacagcc 240
tatatgcagc tcagtagcct gacatttgag gactctgctg tctattttctg tgcaagactg 300
aggaactggg acgagcctat ggactactgg ggccaaggga ccacggtcac cgtctcctca 360
ggtggtggtg gttctggcgg cggcggctcc ggtggtggtg gttctgagct cgtgatgaca 420
cagtctccat cctccctgac tgtgacagca ggagagaagg tcactatgag ctgcaagtcc 480
agtcagagtc tgttaaacag tggaaatcaa aagaactact tgacctggta ccagcagaaa 540
ccagggcagc ctcctaaact gttgatctac tgggcatcca ctagggaatc tggggtcctc 600
gatcgcttca caggcagtgg atctggaaca gatttcactc tcaccatcag cagtgtgcag 660
gctgaagacc tggcagttta ttactgtcag aatgattata gttatccgct cacgttcggt 720
gctgggacca agcttgagat caaatccgga ggtggtggat ccgacgtcca actggtgcag 780
tcaggggctg aagtgaaaaa acctggggcc tcagtgaagg tgtcctgcaa ggcttctggc 840
tacaccttta ctaggtacac gatgcactgg gtaaggcagg cacctggaca gggctctggaa 900
tggtattgat acattaatcc tagccgtggt tataactaatt acgcagacag cgtcaagggc 960
cgcttcacaa tcactacaga caaatccacc agcacagcct acatggaact gagcagcctg 1020
cgttctgagg aactgcaac ctattactgt gcaagatatt atgatgatca ttactgcctt 1080
gactactggg gccaaaggcac cacggtcacc gtctcctcag gcgaagggtac tagtactggt 1140

tctggtggaa gtggagggttc aggtggagca gacgacattg tactgaccca gtctccagca 1200
actctgtctc tgtctccagg ggagcgtgcc accctgagct gcagagccag tcaaagtgtg 1260
agttacatga actggtacca gcagaagccg ggcaaggcac ccaaaagatg gatttatgac 1320
acatccaaag tggcttctgg agtccctgct cgcttcagtg gcagtgggtc tgggaccgac 1380
tactctctca caatcaacag cttggaggct gaagatgctg ccacttatta ctgccaacag 1440
tggagtagta acccgctcac gttcggtggc gggaccaagg tggagatcaa a 1491

<210> 245

<211> 497

<212> PRT

<213> artificial sequence

<220>

<223> 5-10xVH5VL2 HLHL

<400> 245

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
1 5 10 15

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
20 25 30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
35 40 45

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
65 70 75 80

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
85 90 95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser
130 135 140

Ser Leu Thr Val Thr Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser
145 150 155 160

Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu Thr Trp
165 170 175

Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala
180 185 190

Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser
195 200 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu
210 215 220

Ala Val Tyr Tyr Cys Gln Asn Asp Tyr Ser Tyr Pro Leu Thr Phe Gly
225 230 235 240

Ala Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Asp Val
245 250 255

Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val
260 265 270

Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met
275 280 285

His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr
290 295 300

Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly
305 310 315 320

Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu
325 330 335

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg
340 345 350

Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr
355 360 365

Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser
370 375 380

Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser Pro Ala
385 390 395 400

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
405 410 415

Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys
420 425 430

Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val
435 440 445

Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr
450 455 460

Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
465 470 475 480

Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
485 490 495

Lys

<210> 246
<211> 1488
<212> DNA
<213> artificial sequence

<220>
<223> 5-10xVL2VH5 LHLH

<400> 246
gagctcgtga tgacacagtc tccatcctcc ctgactgtga cagcaggaga gaaggctact 60
atgagctgca agtccagtca gagtctgtta aacagtggaa atcaaaagaa ctacttgacc 120
tggtaccagc agaaaccagg gcagcctcct aaactgttga tctactgggc atccactagg 180
gaatctgggg tccctgatcg cttcacaggc agtggatctg gaacagattt cactctcacc 240
atcagcagtg tgcaggctga agacctggca gtttattact gtcagaatga ttatagttat 300
ccgctcacgt tcggtgctgg gaccaagctt gagatcaaag gtgggtgggtg ttctggcggc 360
ggcggctccg gtgggtgggtg ttctgaggtg cagctgctcg agcagtctgg agctgagctg 420
gtaaggcctg ggacttcagt gaagatatcc tgcaaggctt ctggatacgc cttcactaac 480

tactggctag gttgggtaaa gcagaggcct ggacatggac ttgagtggat tggagatatt 540
 ttccctggaa gtggtaatat ccactacaat gagaagttca agggcaaagc cacactgact 600
 gcagacaaat cttcgagcac agcctatatg cagctcagta gcctgacatt tgaggactct 660
 gctgtctatt tctgtgcaag actgaggaac tgggacgagc ctatggacta ctggggccaa 720
 gggaccacgg tcaccgtctc ctccggaggt ggtggatccg acattgtact gacccagtct 780
 ccagcaactc tgtctctgtc tccaggggag cgtgccaccc tgagctgcag agccagtcaa 840
 agtgtaagtt acatgaactg gtaccagcag aagccgggca aggcacccaa aagatggatt 900
 tatgacacat ccaaagtggc ttctggagtc cctgctcgct tcagtggcag tgggtctggg 960
 accgactact ctctcacaat caacagcttg gaggtgaag atgctgccac ttattactgc 1020
 caacagtgga gtagtaaccc gctcacgttc ggtggcggga ccaaggtgga gatcaaaggc 1080
 gaaggtacta gtactgggtc tgggtggaagt ggaggttcag gtggagcaga cgacgtccaa 1140
 ctggtgcagt caggggctga agtgaaaaaa cctggggcct cagtgaaggt gtcctgcaag 1200
 gcttctggct acacctttac taggtacacg atgcactggg taaggcaggc acctggacag 1260
 ggtctggaat ggattggata cattaatcct agccgtgggt atactaatta cgcagacagc 1320
 gtcaagggcc gcttcacaat cactacagac aaatccacca gcacagccta catggaactg 1380
 agcagcctgc gttctgagga cactgcaacc tattactgtg caagatatta tgatgatcat 1440
 tactgccttg actactgggg ccaaggcacc acggtcaccg tctcctca 1488

<210> 247

<211> 496

<212> PRT

<213> artificial sequence

<220>

<223> 5-10xVL2VH5 LHLH

<400> 247

Glu Leu Val Met Thr Gln Ser Pro Ser Ser Leu Thr Val Thr Ala Gly
 1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
 20 25 30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Asp Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile
100 105 110

Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
130 135 140

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
145 150 155 160

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
165 170 175

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
180 185 190

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
195 200 205

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
210 215 220

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
225 230 235 240

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Val
245 250 255

Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
260 265 270

Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr
275 280 285

Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser

290

295

300

Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
305 310 315 320

Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala
325 330 335

Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly
340 345 350

Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr Gly Ser Gly
355 360 365

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu Val Gln Ser
370 375 380

Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys
385 390 395 400

Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln
405 410 415

Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg
420 425 430

Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Thr
435 440 445

Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg
450 455 460

Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His
465 470 475 480

Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
485 490 495

<210> 248

<211> 1491

<212> DNA

<213> artificial sequence

<220>

<223> 5-10xVL2VH5 HLLH

<400> 248

gaggtgcagc tgctcgagca gtctggagct gagctggtaa ggcctgggac ttcagtgaag 60
atatactgca aggccttctgg atacgccttc actaactact ggctaggttg ggtaaagcag 120
aggcctggac atggacttga gtggattgga gatattttcc ctggaagtgg taatatccac 180
tacaatgaga agttcaaggg caaagccaca ctgactgcag acaaattcttc gagcacagcc 240
tatatgcagc tcagtagcct gacatttgag gactctgctg tctattttctg tgcaagactg 300
aggaactggg acgagcctat ggactactgg ggccaaggga ccacggtcac cgtctcctca 360
ggtggtggtg gttctggcgg cggcggctcc ggtggtggtg gttctgagct cgtgatgaca 420
cagtctccat cctccctgac tgtgacagca ggagagaagg tcactatgag ctgcaagtcc 480
agtcagagtc tgttaaacag tggaaatcaa aagaactact tgacctggta ccagcagaaa 540
ccagggcagc ctctaaact gttgatctac tgggcatcca ctagggaatc tggggtcctc 600
gatcgcttca caggcagtgg atctggaaca gatttcactc tcaccatcag cagtgtgcag 660
gctgaagacc tggcagttta ttactgtcag aatgattata gttatccgct cacgttcggt 720
gctgggacca agcttgagat caaatccgga ggtggtggat ccgacattgt actgaccag 780
tctccagcaa ctctgtctct gtctccaggg gagcgtgcca ccctgagctg cagagccagt 840
caaagtgtaa gttacatgaa ctggtaccag cagaagccgg gcaaggcacc caaaagatgg 900
atttatgaca catccaaagt ggcttctgga gtccctgctc gcttcagtgg cagtgggtct 960
gggaccgact actctctcac aatcaacagc ttggaggctg aagatgctgc cacttattac 1020
tgccaacagt ggagtagtaa cccgctcacg ttcggtggcg ggaccaagggt ggagatcaaa 1080
ggcgaaggta ctagtactgg ttctgggtgga agtggagggt cagggtggagc agacgacgtc 1140
caactggtgc agtcaggggc tgaagtgaaa aaacctgggg cctcagtga ggtgtcctgc 1200
aaggcttctg gctacacctt tactaggtac acgatgcact gggtaaggca ggcacctgga 1260
cagggtctgg aatggattgg atacattaat cctagccgtg gttatactaa ttacgcagac 1320
agcgtcaagg gccgcttcac aatcactaca gacaaatcca ccagcacagc ctacatggaa 1380
ctgagcagcc tgcgttctga ggacactgca acctattact gtgcaagata ttatgatgat 1440
cattactgcc ttgactactg gggccaaggc accacggtca ccgtctcctc a 1491

<210> 249

<211> 497

<212> PRT

<213> artificial sequence

<220>

<223> 5-10xVL2VH5 HLLH

<400> 249

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
1 5 10 15

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
20 25 30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
35 40 45

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
65 70 75 80

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
85 90 95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser
130 135 140

Ser Leu Thr Val Thr Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser
145 150 155 160

Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu Thr Trp
165 170 175

Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala
180 185 190

Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser
195 200 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu
210 215 220

Ala Val Tyr Tyr Cys Gln Asn Asp Tyr Ser Tyr Pro Leu Thr Phe Gly
225 230 235 240

Ala Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Asp Ile
245 250 255

Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg
260 265 270

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp
275 280 285

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr
290 295 300

Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser
305 310 315 320

Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala
325 330 335

Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly
340 345 350

Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr Gly Ser
355 360 365

Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu Val Gln
370 375 380

Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys
385 390 395 400

Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg
405 410 415

Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser
420 425 430

Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile
435 440 445

Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu
450 455 460

Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp
465 470 475 480

His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser
485 490 495

Ser

<210> 250
<211> 1488
<212> DNA
<213> artificial sequence

<220>
<223> 5-10 VH5VL3 LHHL

<400> 250
gagctcgtga tgacacagtc tccatcctcc ctgactgtga cagcaggaga gaaggtcact 60
atgagctgca agtccagtca gagtctgtta aacagtggaa atcaaaagaa ctacttgacc 120
tggtaccagc agaaaccagg gcagcctcct aaactgttga tctactgggc atccactagg 180
gaatctgggg tccctgatcg cttcacaggc agtggatctg gaacagattt cactctcacc 240
atcagcagtg tgcaggctga agacctggca gtttattact gtcagaatga ttatagttat 300
ccgctcacgt tcggtgctgg gaccaagctt gagatcaaag gtggtggtgg ttctggcggc 360
ggcggctccg gtggtggtgg ttctgaggtg cagctgctcg agcagtctgg agctgagctg 420
gtaaggcctg ggacttcagt gaagatatcc tgcaaggctt ctggatacgc cttcactaac 480
tactggctag gttgggtaaa gcagaggcct ggacatggac ttgagtggat tggagatatt 540
ttccctggaa gtggtaatat ccactacaat gagaagttca agggcaaagc cacactgact 600
gcagacaaat cttcgagcac agcctatatg cagctcagta gcctgacatt tgaggactct 660
gctgtctatt tctgtgcaag actgaggaac tgggacgagc ctatggacta ctggggccaa 720
gggaccacgg tcaccgtctc ctccggaggt ggtggatccg acgtccaact ggtgcagtca 780
ggggctgaag tgaaaaaacc tggggcctca gtgaaggtgt cctgcaaggc ttctggctac 840
acctttacta ggtacacgat gcactgggta aggcaggcac ctggacaggg tctggaatgg 900
attggataca ttaatcctag ccgtggttat actaattacg cagacagcgt caagggccgc 960
ttcacaatca ctacagacaa atccaccagc acagcctaca tggaactgag cagcctgcgt 1020
tctgaggaca ctgcaaccta ttactgtgca agatattatg atgatcatta ctgccttgac 1080
tactggggcc aaggcaccac ggtcaccgtc tcctcaggcg aaggtactag tactggttct 1140

ggtggaagtg gaggttcagg tggagcagac gacattgtac tgaccagtc tccagcaact 1200
 ctgtctctgt ctccagggga gcgtgccacc ctgacctgca gagccagttc aagtgttaagt 1260
 tacatgaact ggtaccagca gaagccgggc aaggcaccga aaagatggat ttatgacaca 1320
 tccaaagtgg cttctggagt ccctgctcgc ttcagtggca gtgggtcttg gaccgactac 1380
 tctctcacia tcaacagctt ggaggctgaa gatgctgcca cttattactg ccaacagtgg 1440
 agtagtaacc cgctcacgtt cggtggcggg accaaggtgg agatcaaa 1488

<210> 251

<211> 496

<212> PRT

<213> artificial sequence

<220>

<223> 5-10VH5VL3 LHHL

<400> 251

Glu Leu Val Met Thr Gln Ser Pro Ser Ser Leu Thr Val Thr Ala Gly
 1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
 20 25 30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Asn
 85 90 95

Asp Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile
 100 105 110

Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 115 120 125

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
 130 135 140

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
145 150 155 160

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
165 170 175

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
180 185 190

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
195 200 205

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
210 215 220

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
225 230 235 240

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Val Gln
245 250 255

Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys
260 265 270

Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His
275 280 285

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile
290 295 300

Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg
305 310 315 320

Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu
325 330 335

Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr
340 345 350

Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val
355 360 365

Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser Gly
370 375 380

Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser Pro Ala Thr
385 390 395 400

Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys Arg Ala Ser
405 410 415

Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
420 425 430

Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro
435 440 445

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
450 455 460

Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
465 470 475 480

Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
485 490 495

<210> 252
<211> 1491
<212> DNA
<213> artificial sequence

<220>
<223> 5-10VH5VL3 HLHL

<400> 252
gaggtgcagc tgctcgagca gtctggagct gagctggtaa ggcctgggac ttcagtgaag 60
atatacctgca aggcttctgg atacgccttc actaactact ggctaggttg ggtaaagcag 120
aggcctggac atggacttga gtggattgga gatattttcc ctggaagtgg taatatccac 180
tacaatgaga agttcaaggg caaagccaca ctgactgcag acaaattctc gagcacagcc 240
tatatgcagc tcagtagcct gacatttgag gactctgctg tctattttctg tgcaagactg 300
aggaactggg acgagcctat ggactactgg ggccaaggga ccacggtcac cgtctcctca 360
ggtggtggtg gttctggcgg cggcggctcc ggtggtggtg gttctgagct cgtgatgaca 420
cagtctccat cctccctgac tgtgacagca ggagagaagg tcactatgag ctgcaagtcc 480
agtcagagtc tgtaaacag tggaaatcaa aagaactact tgacctggta ccagcagaaa 540
ccagggcagc ctctaaact gttgatctac tgggcatcca ctagggaatc tggggtcct 600

gatcgcttca caggcagtgg atctggaaca gatttcactc tcaccatcag cagtgtgcag 660
gctgaagacc tggcagttta ttactgtcag aatgattata gttatccgct cacgttcggt 720
gctgggacca agcttgagat caaatccgga ggtggtggat ccgacgtcca actggtgcag 780
tcaggggctg aagtgaaaaa acctggggcc tcagtgaagg tgtcctgcaa ggcttctggc 840
tacaccttta ctaggtacac gatgcactgg gtaaggcagg cacctggaca gggctctggaa 900
tggtattgat acattaatcc tagccgtggt tatactaatt acgcagacag cgtcaagggc 960
cgcttcacaa tcactacaga caaatccacc agcacagcct acatggaact gagcagcctg 1020
cgcttctgagg aactgcaac ctattactgt gcaagatatt atgatgatca ttactgcctt 1080
gactactggg gccaaaggcac cacggtcacc gtctcctcag gcgaaggtag tagtactggt 1140
tctggtggaa gtggaggttc aggtggagca gacgacattg tactgacca gtctccagca 1200
actctgtctc tgtctccagg ggagcgtgcc accctgacct gcagagccag ttcaagtgta 1260
agttacatga actggtacca gcagaagccg ggcaaggcac caaaagatg gatttatgac 1320
acatccaaag tggcttctgg agtccttctg cgcttcagtg gcagtgggtc tgggaccgac 1380
tactctctca caatcaacag cttggaggct gaagatgctg ccacttatta ctgccaacag 1440
tggagtagta acccgctcac gttcggtggc gggaccaagg tggagatcaa a 1491

<210> 253
<211> 497
<212> PRT
<213> artificial sequence

<220>
<223> 5-10VH5VL3 HLHL

<400> 253

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
1 5 10 15

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
20 25 30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
35 40 45

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
65 70 75 80

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
85 90 95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser
130 135 140

Ser Leu Thr Val Thr Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser
145 150 155 160

Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu Thr Trp
165 170 175

Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala
180 185 190

Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser
195 200 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu
210 215 220

Ala Val Tyr Tyr Cys Gln Asn Asp Tyr Ser Tyr Pro Leu Thr Phe Gly
225 230 235 240

Ala Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Asp Val
245 250 255

Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val
260 265 270

Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met
275 280 285

His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr
290 295 300

Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly

305					310					315					320
Arg	Phe	Thr	Ile	Thr	Thr	Asp	Lys	Ser	Thr	Ser	Thr	Ala	Tyr	Met	Glu
				325					330					335	
Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Thr	Tyr	Tyr	Cys	Ala	Arg
			340					345					350		
Tyr	Tyr	Asp	Asp	His	Tyr	Cys	Leu	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Thr
		355					360					365			
Val	Thr	Val	Ser	Ser	Gly	Glu	Gly	Thr	Ser	Thr	Gly	Ser	Gly	Gly	Ser
	370					375					380				
Gly	Gly	Ser	Gly	Gly	Ala	Asp	Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala
385					390					395					400
Thr	Leu	Ser	Leu	Ser	Pro	Gly	Glu	Arg	Ala	Thr	Leu	Thr	Cys	Arg	Ala
				405					410					415	
Ser	Ser	Ser	Val	Ser	Tyr	Met	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys
			420					425					430		
Ala	Pro	Lys	Arg	Trp	Ile	Tyr	Asp	Thr	Ser	Lys	Val	Ala	Ser	Gly	Val
		435					440					445			
Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Tyr	Ser	Leu	Thr
	450					455					460				
Ile	Asn	Ser	Leu	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln
465					470					475					480
Trp	Ser	Ser	Asn	Pro	Leu	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile
				485					490					495	

Lys

<210>	254
<211>	1488
<212>	DNA
<213>	artificial sequence

<220>
<223> 5-10VL3VH5 LHLH

<400> 254

gagctcgtga tgacacagtc tccatcctcc ctgactgtga cagcaggaga gaaggtcact	60
atgagctgca agtccagtca gagtctgtta aacagtggaa atcaaaagaa ctacttgacc	120
tggtaccagc agaaaccagg gcagcctcct aaactgttga tctactgggc atccactagg	180
gaatctgggg tccctgatcg cttcacaggc agtggatctg gaacagattt cactctcacc	240
atcagcagtg tgcaggctga agacctggca gtttattact gtcagaatga ttatagttat	300
ccgctcacgt tcggtgctgg gaccaagctt gagatcaaag gtggtggtgg ttctggcggc	360
ggcggctccg gtggtggtgg ttctgaggtg cagctgctcg agcagtctgg agctgagctg	420
gtaaggcctg ggacttcagt gaagatatcc tgcaaggctt ctggatacgc cttcactaac	480
tactggctag gttgggtaaa gcagaggcct ggacatggac ttgagtggat tggagatatt	540
ttccctggaa gtggtaatat ccactacaat gagaagttca agggcaaagc cacactgact	600
gcagacaaat cttcgagcac agcctatatg cagctcagta gcctgacatt tgaggactct	660
gctgtctatt tctgtgcaag actgaggaac tgggacgagc ctatggacta ctggggccaa	720
gggaccacgg tcaccgtctc ctccggaggt ggtggatccg acattgtact gacccagtct	780
ccagcaactc tgtctctgtc tccaggggag cgtgccaccc tgacctgcag agccagttca	840
agtgtgaagt acatgaactg gtaccagcag aagccgggca aggcacccaa aagatggatt	900
tatgacacat ccaaagtggc ttctggagtc cctgctcgct tcagtggcag tgggtctggg	960
accgactact ctctcacaat caacagcttg gaggtgaag atgctgccac ttattactgc	1020
caacagtgga gtagtaaccc gctcacgttc ggtggcgggg ccaagggtgga gatcaaaggc	1080
gaaggtaacta gtactggttc tgggtggaagt ggaggttcag gtggagcaga cgacgtccaa	1140
ctggtgcagt caggggctga agtgaaaaaa cctggggcct cagtgaagggt gtcctgcaag	1200
gcttctggct acacctttac taggtacacg atgcactggg taaggcaggc acctggacag	1260
ggtctggaat ggattggata cattaatcct agccgtgggt atactaatta cgcagacagc	1320
gtcaagggcc gcttcacaat cactacagac aaatccacca gcacagccta catggaactg	1380
agcagcctgc gttctgagga cactgcaacc tattactgtg caagatatta tgatgatcat	1440
tactgccttg actactgggg ccaaggcacc acggtcaccg tctcctca	1488

<210> 255

<211> 496

<212> PRT

<213> artificial sequence

<220>

<223> 5-10VL3VH5 LHLH

<400> 255

Glu Leu Val Met Thr Gln Ser Pro Ser Ser Leu Thr Val Thr Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Asp Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile
100 105 110

Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
130 135 140

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
145 150 155 160

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
165 170 175

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
180 185 190

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
195 200 205

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
210 215 220

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
 225 230 235 240

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Val
 245 250 255

Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
 260 265 270

Thr Leu Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr
 275 280 285

Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser
 290 295 300

Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
 305 310 315 320

Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala
 325 330 335

Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly
 340 345 350

Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr Gly Ser Gly
 355 360 365

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu Val Gln Ser
 370 375 380

Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys
 385 390 395 400

Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln
 405 410 415

Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg
 420 425 430

Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Thr
 435 440 445

Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg
 450 455 460

Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His
 465 470 475 480

Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 485 490 495

<210> 256
 <211> 1491
 <212> DNA
 <213> artificial sequence

<220>
 <223> 5-10VL3VH5 HLLH

<400> 256
 gaggtgcagc tgctcgagca gtctggagct gagctggtaa ggcctgggac ttcagtgaag 60
 atatcctgca aggcttctgg atacgccttc actaactact ggctaggttg ggtaaagcag 120
 aggcctggac atggacttga gtggattgga gatattttcc ctggaagtgg taatatccac 180
 tacaatgaga agttcaaggg caaagccaca ctgactgcag acaaatcttc gagcacagcc 240
 tatatgcagc tcagtagcct gacatttgag gactctgctg tctatttctg tgcaagactg 300
 aggaactggg acgagcctat ggactactgg ggccaaggga ccacggtcac cgtctcctca 360
 ggtgggtggg gttctggcgg cggcggctcc ggtgggtggg gttctgagct cgtgatgaca 420
 cagtctccat cctccctgac tgtgacagca ggagagaagg tcactatgag ctgcaagtcc 480
 agtcagagtc tgtaaacag tggaaatcaa aagaactact tgacctggta ccagcagaaa 540
 ccagggcagc ctctaaact gttgatctac tgggcatcca ctagggaatc tggggtcctt 600
 gatcgcttca caggcagtgg atctggaaca gatttcactc tcaccatcag cagtgtgcag 660
 gctgaagacc tggcagttta ttactgtcag aatgattata gttatccgct cacgttcggg 720
 gctgggacca agcttgagat caaatccgga ggtgggtggat ccgacattgt actgaccag 780
 tctccagcaa ctctgtctct gtctccaggg gagcgtgcc aactgacctg cagagccagt 840
 tcaagtgtaa gttacatgaa ctgggtaccag cagaagccgg gcaaggcacc caaagatgg 900
 atttatgaca catcaaagt ggcttctgga gtccctgctc gcttcagtgg cagtgggtct 960
 gggaccgact actctctcac aatcaacagc ttggaggctg aagatgctgc cacttattac 1020
 tgccaacagt ggagtagtaa cccgctcacg ttcgggtggc ggaccaagggt ggagatcaaa 1080
 ggcgaaggta ctagtactgg ttctgggtgga agtgagggtt caggtggagc agacgacgtc 1140
 caactgggtgc agtcaggggc tgaagtgaaa aaacctgggg cctcagtga ggtgtcctgc 1200
 aaggcttctg gctacacctt tactaggtac acgatgcact gggtaaggca ggcacctgga 1260

cagggctctgg aatggattgg atacattaat cctagccgtg gttataactaa ttacgcagac 1320
agcgtcaagg gccgcttcac aatcactaca gacaaatcca ccagcacagc ctacatggaa 1380
ctgagcagcc tgcgttctga ggacactgca acctattact gtgcaagata ttatgatgat 1440
cattactgcc ttgactactg gggccaaggc accacgggtca ccgtctcctc a 1491

<210> 257
<211> 497
<212> PRT
<213> artificial sequence

<220>
<223> 5-10VL3VH5 HLLH

<400> 257

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
1 5 10 15

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
20 25 30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
35 40 45

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
65 70 75 80

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
85 90 95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser
130 135 140

Ser Leu Thr Val Thr Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser
145 150 155 160

Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu Thr Trp
 165 170 175

Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala
 180 185 190

Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser
 195 200 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu
 210 215 220

Ala Val Tyr Tyr Cys Gln Asn Asp Tyr Ser Tyr Pro Leu Thr Phe Gly
 225 230 235 240

Ala Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Asp Ile
 245 250 255

Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg
 260 265 270

Ala Thr Leu Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp
 275 280 285

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr
 290 295 300

Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Ser Gly Ser
 305 310 315 320

Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala
 325 330 335

Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly
 340 345 350

Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr Gly Ser
 355 360 365

Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu Val Gln
 370 375 380

Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys
 385 390 395 400

Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg
405 410 415

Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser
420 425 430

Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile
435 440 445

Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu
450 455 460

Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp
465 470 475 480

His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser
485 490 495

Ser

<210> 258
<211> 1488
<212> DNA
<213> artificial sequence

<220>
<223> 5-10VH7VL1 LHHL

<400> 258
gagctcgtga tgacacagtc tccatcctcc ctgactgtga cagcaggaga gaaggtcact 60
atgagctgca agtccagtca gagtctgtta aacagtggaa atcaaaagaa ctacttgacc 120
tggtaccagc agaaaccagg gcagcctcct aaactggtga tctactgggc atccactagg 180
gaatctgggg tccctgatcg cttcacaggc agtggatctg gaacagattt cactctcacc 240
atcagcagtg tgcaggctga agacctggca gtttattact gtcagaatga ttatagttat 300
ccgctcacgt tcggtgctgg gaccaagctt gagatcaaag gtggtggtgg ttctggcggc 360
ggcggtccg gtggtggtgg ttctgaggtg cagctgctcg agcagtctgg agctgagctg 420
gtaaggcctg ggacttcagt gaagatatcc tgcaaggctt ctggatacgc cttcactaac 480
tactggctag gttgggtaaa gcagaggcct ggacatggac ttgagtggat tggagatatt 540
ttccctggaa gtggtaatat ccactacaat gagaagttca agggcaaagc cacactgact 600

gcagacaaat cttcgagcac agcctatatg cagctcagta gcctgacatt tgaggactct 660
gctgtctatt tctgtgcaag actgaggaac tgggacgagc ctatggacta ctggggccaa 720
gggaccacgg tcaccgtctc ctccggaggt ggtggatccg acgtccaact ggtgcagtca 780
ggggctgaag tgaaaaaacc tggggcctca gtgaagggtgt cctgcaaggc ttctggctac 840
acctttacta ggtacacgat gcactgggta aggcaggcac ctggacaggg tctggaatgg 900
attggataca ttaatcctag ccgtgggttat actaattaca atcagaagtt caaggaccgc 960
gtcacaatca ctacagacaa atccaccagc acagcctaca tggaactgag cagcctgcgt 1020
tctgaggaca ctgcagtcta ttactgtgca agatattatg atgatcatta ctgccttgac 1080
tactggggcc aaggcaccac ggtcacccgc tctcaggcg aaggtactag tactggttct 1140
ggtggaagtg gaggttcagg tggagcagac gacattcaga tgaccagtc tccatctagc 1200
ctgtctgcat ctgtcgggga ccgtgtcacc atcacctgca gagccagtca aagtgtagt 1260
tacatgaact ggtaccagca gaagccgggc aaggcaccca aaagatggat ttatgacaca 1320
tccaaagtgg cttctggagt ccctgctcgc ttcagtggca gtgggtctgg gaccgactac 1380
tctctcacia tcaacagctt ggaggctgaa gatgctgcc a ttattactg ccaacagtgg 1440
agtagtaacc cgctcacgtt cggtggcggg accaaggtgg agatcaaa 1488

<210> 259
<211> 496
<212> PRT
<213> artificial sequence

<220>
<223> 5-10VH7VL1 LHHL

<400> 259

Glu Leu Val Met Thr Gln Ser Pro Ser Ser Leu Thr Val Thr Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Asp Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile
100 105 110

Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
130 135 140

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
145 150 155 160

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
165 170 175

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
180 185 190

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
195 200 205

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
210 215 220

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
225 230 235 240

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Val Gln
245 250 255

Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys
260 265 270

Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His
275 280 285

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile
290 295 300

Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg

305 310 315 320

Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu
 325 330 335

Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr
 340 345 350

Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val
 355 360 365

Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser Gly
 370 375 380

Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
385 390 395 400

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
 405 410 415

Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
 420 425 430

Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro
 435 440 445

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
 450 455 460

Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
465 470 475 480

Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 485 490 495

<210> 260
<211> 1491
<212> DNA
<213> artificial sequence

<220>
<223> 5-10VH7VL1 HLHL

<400> 260
gaggtgcagc tgctcgagca gtctggagct gagctggtaa ggcctgggac ttcagtgaag 60
atatcctgca aggcttctgg atacgccttc actaactact ggctaggttg ggtaaagcag 120

aggcctggac atggacttga gtggattgga gatattttcc ctggaagtgg taatatccac 180
tacaatgaga agttcaaggg caaagccaca ctgactgcag acaaattctc gagcacagcc 240
tatatgcagc tcagtagcct gacatttgag gactctgctg tctattttctg tgcaagactg 300
aggaactggg acgagcctat ggactactgg ggccaaggga ccacggtcac cgtctcctca 360
ggtggtggtg gttctggcgg cggcggctcc ggtggtggtg gttctgagct cgtgatgaca 420
cagtctccat cctccctgac tgtgacagca ggagagaagg tcactatgag ctgcaagtcc 480
agtcagagtc tgttaaacag tggaaatcaa aagaactact tgacctggta ccagcagaaa 540
ccagggcagc ctccctaaact gttgatctac tgggcatcca ctagggaatc tggggtcctc 600
gatcgcttca caggcagtgg atctggaaca gatttcactc tcaccatcag cagtgtgcag 660
gctgaagacc tggcagttta ttactgtcag aatgattata gttatccgct cacgttcggt 720
gctgggacca agcttgagat caaatccgga ggtggtggat ccgacgtcca actggtgcag 780
tcaggggctg aagtgaaaaa acctggggcc tcagtgaagg tgtcctgcaa ggcttctggc 840
tacaccttta ctaggtacac gatgcactgg gtaaggcagg cacctggaca gggctctggaa 900
tggattggat acattaatcc tagccgtggt tataactaatt acaatcagaa gttcaaggac 960
cgcgtcacaa tcactacaga caaatccacc agcacagcct acatggaact gagcagcctg 1020
cgttctgagg aactgcagt ctattactgt gcaagatatt atgatgatca ttactgcctt 1080
gactactggg gccaaggcac cacggtcacc gtctcctcag gcgaaggtag tagtactggt 1140
tctggtggaa gtggaggttc aggtggagca gacgacattc agatgacca gtctccatct 1200
agcctgtctg catctgtcgg ggaccgtgtc accatcacct gcagagccag tcaaagtgtg 1260
agttacatga actggtacca gcagaagccg ggcaaggcac ccaaaagatg gatttatgac 1320
acatccaaag tggcttctgg agtccctgct cgcttcagtg gcagtgggtc tgggaccgac 1380
tactctctca caatcaacag cttggaggct gaagatgctg ccacttatta ctgccaacag 1440
tggagtagta acccgctcac gttcggtggc gggaccaagg tggagatcaa a 1491

<210> 261

<211> 497

<212> PRT

<213> artificial sequence

<220>

<223> 5-10VH7VL1 HLHL

<400> 261

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly

1	5	10	15												
Thr	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ala	Phe	Thr	Asn
			20					25					30		
Tyr	Trp	Leu	Gly	Trp	Val	Lys	Gln	Arg	Pro	Gly	His	Gly	Leu	Glu	Trp
		35					40					45			
Ile	Gly	Asp	Ile	Phe	Pro	Gly	Ser	Gly	Asn	Ile	His	Tyr	Asn	Glu	Lys
	50					55					60				
Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	Ser	Ser	Ser	Thr	Ala
65					70					75					80
Tyr	Met	Gln	Leu	Ser	Ser	Leu	Thr	Phe	Glu	Asp	Ser	Ala	Val	Tyr	Phe
				85					90					95	
Cys	Ala	Arg	Leu	Arg	Asn	Trp	Asp	Glu	Pro	Met	Asp	Tyr	Trp	Gly	Gln
			100					105					110		
Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly
		115					120					125			
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Glu	Leu	Val	Met	Thr	Gln	Ser	Pro	Ser
	130					135					140				
Ser	Leu	Thr	Val	Thr	Ala	Gly	Glu	Lys	Val	Thr	Met	Ser	Cys	Lys	Ser
145					150					155					160
Ser	Gln	Ser	Leu	Leu	Asn	Ser	Gly	Asn	Gln	Lys	Asn	Tyr	Leu	Thr	Trp
			165						170					175	
Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala
			180					185					190		
Ser	Thr	Arg	Glu	Ser	Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly	Ser	Gly	Ser
		195					200					205			
Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Val	Gln	Ala	Glu	Asp	Leu
	210					215					220				
Ala	Val	Tyr	Tyr	Cys	Gln	Asn	Asp	Tyr	Ser	Tyr	Pro	Leu	Thr	Phe	Gly
225					230					235					240

Ala Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Asp Val
245 250 255

Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val
260 265 270

Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met
275 280 285

His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr
290 295 300

Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp
305 310 315 320

Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu
325 330 335

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
340 345 350

Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr
355 360 365

Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser
370 375 380

Gly Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser Pro Ser
385 390 395 400

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
405 410 415

Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys
420 425 430

Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val
435 440 445

Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr
450 455 460

Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
465 470 475 480

Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
 485 490 495

Lys

<210> 262
 <211> 1488
 <212> DNA
 <213> artificial sequence

<220>
 <223> 5-10VL1VH7 LHLH

<400> 262
 gagctcgtga tgacacagtc tccatcctcc ctgactgtga cagcaggaga gaaggtcact 60
 atgagctgca agtccagtca gagtctgtta aacagtggaa atcaaaagaa ctacttgacc 120
 tgggtaccagc agaaaccagg gcagcctcct aaactgttga tctactgggc atccactagg 180
 gaatctgggg tccctgatcg cttcacaggc agtggatctg gaacagattt cactctcacc 240
 atcagcagtg tgcaggctga agacctggca gtttattact gtcagaatga ttatagttat 300
 ccgctcacgt tcggtgctgg gaccaagctt gagatcaaag gtggtggtgg ttctggcggc 360
 ggcggtccg gtggtggtgg ttctgaggtg cagctgctcg agcagtctgg agctgagctg 420
 gtaaggcctg ggacttcagt gaagatatcc tgcaaggctt ctggatacgc cttcactaac 480
 tactggctag gttgggtaaa gcagaggcct ggacatggac ttgagtggat tggagatatt 540
 ttccctggaa gtggtaatat ccactacaat gagaagttca agggcaaagc cacactgact 600
 gcagacaaat cttcgagcac agcctatatg cagctcagta gcctgacatt tgaggactct 660
 gctgtctatt tctgtgcaag actgaggaac tgggacgagc ctatggacta ctggggccaa 720
 gggaccacgg tcaccgtctc ctccggaggt ggtggatccg acattcagat gaccagctct 780
 ccatctagcc tgtctgcac tgctggggac cgtgtcacca tcacctgcag agccagtcaa 840
 agtgtaagtt acatgaactg gtaccagcag aagccgggca aggcacccaa aagatggatt 900
 tatgacacat ccaaagtggc ttctggagtc cctgctcgct tcagtggcag tgggtctggg 960
 accgactact ctctcacaat caacagcttg gaggtgaag atgctgccac ttattactgc 1020
 caacagtgga gtagtaacct gctcacgttc ggtggcgagg ccaaggtgga gatcaaaggc 1080
 gaaggtacta gtactgggtc tgggtggaagt ggaggttcag gtggagcaga cgacgtccaa 1140
 ctggtgcagt caggggctga agtgaaaaaa cctggggcct cagtgaaggt gtcctgcaag 1200
 gcttctggct acacctttac taggtacacg atgcactggg taaggcaggc acctggacag 1260

ggtctggaat ggattggata cattaatcct agccgtgggtt atactaatta caatcagaag 1320
 ttcaaggacc gcgtcacaat cactacagac aaatccacca gcacagccta catggaactg 1380
 agcagcctgc gttctgagga cactgcagtc tattactgtg caagatatta tgatgatcat 1440
 tactgccttg actactgggg ccaaggcacc acggtcaccg tctcctca 1488

<210> 263
 <211> 496
 <212> PRT
 <213> artificial sequence

<220>
 <223> 5-10VL1VH7 LHLH

<400> 263

Glu Leu Val Met Thr Gln Ser Pro Ser Ser Leu Thr Val Thr Ala Gly
 1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
 20 25 30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Asn
 85 90 95

Asp Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile
 100 105 110

Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 115 120 125

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
 130 135 140

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
 145 150 155 160

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
 165 170 175

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
 180 185 190

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
 195 200 205

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
 210 215 220

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
 225 230 235 240

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Gln
 245 250 255

Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
 260 265 270

Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr
 275 280 285

Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser
 290 295 300

Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
 305 310 315 320

Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala
 325 330 335

Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly
 340 345 350

Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr Gly Ser Gly
 355 360 365

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu Val Gln Ser
 370 375 380

Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys
 385 390 395 400

Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln
405 410 415

Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg
420 425 430

Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr
435 440 445

Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg
450 455 460

Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His
465 470 475 480

Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
485 490 495

<210> 264

<211> 1491

<212> DNA

<213> artificial sequence

<220>

<223> 5-10VL1VH7 HLLH

<400> 264

gaggtgcagc tgctcgagca gtctggagct gagctggtaa ggcctgggac ttcagtgaag 60
atatactgca aggcttctgg atacgccttc actaactact ggctagggtg ggtaaagcag 120
aggcctggac atggacttga gtggattgga gatattttcc ctggaagtgg taatatccac 180
tacaatgaga agttcaaggg caaagccaca ctgactgcag acaaactctc gagcacagcc 240
tatatgcagc tcagtagcct gacatttgag gactctgctg tctatttctg tgcaagactg 300
aggaactggg acgagcctat ggactactgg ggccaaggga ccacggtcac cgtctcctca 360
ggtggtggtg gttctggcgg cggcggctec ggtggtggtg gttctgagct cgtgatgaca 420
cagtctccat cctccctgac tgtgacagca ggagagaagg tcactatgag ctgcaagtcc 480
agtcagagtc tgtaaacag tggaaatcaa aagaactact tgacctggtg ccagcagaaa 540
ccagggcagc ctctaaact gttgatctac tgggcatcca ctagggaatc tggggtcctc 600
gatcgcttca caggcagtgg atctggaaca gatttcactc tcaccatcag cagtgtgcag 660
gctgaagacc tggcagttta ttactgtcag aatgattata gttatccgct cacgttcggt 720

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gctgggacca agcttgagat caaatccgga ggtgggtggat ccgacattca gatgacccag 780
tctccatcta gcctgtctgc atctgtcggg gaccgtgtca ccatacctg cagagccagt 840
caaagtgtaa gttacatgaa ctggtaccag cagaagccgg gcaaggcacc caaaagatgg 900
atttatgaca catccaaagt ggcttctgga gtccctgctc gcttcagtgg cagtgggtct 960
gggaccgact actctctcac aatcaacagc ttggaggctg aagatgctgc cacttattac 1020
tgccaacagt ggagtagtaa cccgctcacg ttcgggtggcg ggaccaaggt ggagatcaaa 1080
ggcgaaggta ctagtactgg ttctgggtgga agtggagggt caggtggagc agacgacgtc 1140
caactgggtgc agtcaggggc tgaagtga aaacctgggg cctcagtga ggtgtcctgc 1200
aaggcttctg gctacacctt tactaggtac acgatgcact gggtaaggca ggcacctgga 1260
caggggtctgg aatggattgg atacattaat cctagccgtg gttatactaa ttacaatcag 1320
aagttcaagg accgcgtcac aatcactaca gacaaatcca ccagcacagc ctacatggaa 1380
ctgagcagcc tgcgttctga ggacactgca gtctattact gtgcaagata ttatgatgat 1440
cattactgcc ttgactactg gggccaaggc accacgggtca ccgtctcctc a 1491

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<210> 265
<211> 497
<212> PRT
<213> artificial sequence

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<220>
<223> 5-10VL1VH7 HLLH

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<400> 265

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Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
1          5          10          15

```

```

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
20          25          30

```

```

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
35          40          45

```

```

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
50          55          60

```

```

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
65          70          75          80

```

```

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
85          90          95

```

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser
 130 135 140

Ser Leu Thr Val Thr Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser
 145 150 155 160

Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu Thr Trp
 165 170 175

Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala
 180 185 190

Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser
 195 200 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu
 210 215 220

Ala Val Tyr Tyr Cys Gln Asn Asp Tyr Ser Tyr Pro Leu Thr Phe Gly
 225 230 235 240

Ala Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Asp Ile
 245 250 255

Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
 260 265 270

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp
 275 280 285

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr
 290 295 300

Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser
 305 310 315 320

Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala

325

330

335

Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly
 340 345 350

Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr Gly Ser
 355 360 365

Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu Val Gln
 370 375 380

Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys
 385 390 395 400

Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg
 405 410 415

Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser
 420 425 430

Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile
 435 440 445

Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu
 450 455 460

Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp
 465 470 475 480

His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser
 485 490 495

Ser

<210> 266
 <211> 1488
 <212> DNA
 <213> artificial sequence

<220>
 <223> 5-10/VH7VL2 LHHL

<400> 266
 gagctcgtga tgacacagtc tccatcctcc ctgactgtga cagcaggaga gaaggtcact 60
 atgagctgca agtccagtca gagtctgtta aacagtggaa atcaaaagaa ctacttgacc 120

tggtaccagc agaaaccagg gcagcctcct aaactgttga tctactgggc atccactagg 180
gaatctgggg tccctgatcg cttcacaggc agtggatctg gaacagattt cactctcacc 240
atcagcagtg tgcaggctga agacctggca gtttattact gtcagaatga ttatagttat 300
ccgctcacgt tcggtgctgg gaccaagctt gagatcaaag gtggtggtgg ttctggcggc 360
ggcggctccg gtggtggtgg ttctgaggtg cagctgctcg agcagtctgg agctgagctg 420
gtaaggcctg ggacttcagt gaagatatcc tgcaaggctt ctggatacgc cttcactaac 480
tactggctag gttgggtaaa gcagaggcct ggacatggac ttgagtggat tggagatatt 540
ttccctggaa gtggtaatat ccactacaat gagaagttca agggcaaagc cacactgact 600
gcagacaaat cttcgagcac agcctatatg cagctcagta gcctgacatt tgaggactct 660
gctgtctatt tctgtgcaag actgaggaac tgggacgagc ctatggacta ctggggccaa 720
gggaccacgg tcaccgtctc ctccggaggt ggtggatccg acgtccaact ggtgcagtca 780
ggggctgaag tgaaaaaacc tggggcctca gtgaaggtgt cctgcaaggc ttctggctac 840
acctttacta ggtacacgat gcactgggta aggcaggcac ctggacaggg tctggaatgg 900
attggataca ttaatcctag ccgtgggttat actaattaca atcagaagtt caaggaccgc 960
gtcacaatca ctacagacaa atccaccagc acagcctaca tggaaactgag cagcctgcgt 1020
tctgaggaca ctgcagtcta ttactgtgca agatattatg atgatcatta ctgccttgac 1080
tactggggcc aaggcaccac ggtcaccgtc tcctcaggcg aaggtagtag tactggttct 1140
ggtggaagtg gaggttcagg tggagcagac gacattgtac tgaccagtc tccagcaact 1200
ctgtctctgt ctccagggga gcgtgccacc ctgagctgca gagccagtca aagtgttaagt 1260
tacatgaact ggtaccagca gaagccgggc aaggcaccca aaagatggat ttatgacaca 1320
tccaaagtgg cttctggagt ccctgctcgc ttcagtggca gtgggtctgg gaccgactac 1380
tctctcacia tcaacagctt ggaggctgaa gatgctgcca cttattactg ccaacagtgg 1440
agtagtaacc cgctcacgtt cggtggcggg accaaggtgg agatcaaa 1488

<210> 267
<211> 496
<212> PRT
<213> artificial sequence

<220>
<223> 5-10/VH7VL2 LHHL

<400> 267

Glu Leu Val Met Thr Gln Ser Pro Ser Ser Leu Thr Val Thr Ala Gly

1	5	10	15
Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser	20	25	30
Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln	35	40	45
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val	50	55	60
Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr	65	70	75
Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Asn	85	90	95
Asp Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile	100	105	110
Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser	115	120	125
Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly	130	135	140
Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn	145	150	155
Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp	165	170	175
Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys	180	185	190
Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala	195	200	205
Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe	210	215	220
Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln	225	230	235
			240

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Val Gln
245 250 255

Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys
260 265 270

Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His
275 280 285

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile
290 295 300

Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg
305 310 315 320

Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu
325 330 335

Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr
340 345 350

Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val
355 360 365

Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser Gly
370 375 380

Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser Pro Ala Thr
385 390 395 400

Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser
405 410 415

Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
420 425 430

Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro
435 440 445

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
450 455 460

Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
465 470 475 480

Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
485 490 495

<210> 268

<211> 1491

<212> DNA

<213> artificial sequence

<220>

<223> 5-10/VH7VL2 HLHL

<400> 268

gaggtgcagc	tgctcgagca	gtctggagct	gagctggtaa	ggcctgggac	ttcagtgaag	60
atatcctgca	aggcttctgg	atacgccttc	actaactact	ggctaggttg	ggtaaagcag	120
aggcctggac	atggacttga	gtggattgga	gataatttcc	ctggaagtgg	taatatccac	180
tacaatgaga	agttcaaggg	caaagccaca	ctgactgcag	acaaatcttc	gagcacagcc	240
tatatgcagc	tcagtagcct	gacatttgag	gactctgctg	tctatttctg	tgcaagactg	300
aggaactggg	acgagcctat	ggactactgg	ggccaaggga	ccacggtcac	cgtctcctca	360
ggtggtggtg	gttctggcgg	cggcggctcc	ggtggtggtg	gttctgagct	cgtgatgaca	420
cagtctccat	cctccctgac	tgtgacagca	ggagagaagg	tcactatgag	ctgcaagtcc	480
agtcagagtc	tgttaaacag	tggaaatcaa	aagaactact	tgacctggta	ccagcagaaa	540
ccagggcagc	ctcctaaact	gttgatctac	tgggcatcca	ctaggggaatc	tgggggtccct	600
gacgccttca	caggcagtgg	atctggaaca	gatttcactc	tcaccatcag	cagtgtgcag	660
gctgaagacc	tggcagttta	ttactgtcag	aatgattata	gttatccgct	cacgttcggt	720
gctgggacca	agcttgagat	caaatccgga	ggtggtggat	ccgacgtcca	actggtgcag	780
tcaggggctg	aagtgaaaaa	acctggggcc	tcagtgaagg	tgtcctgcaa	ggcttctggc	840
tacaccttta	ctaggtacac	gatgcactgg	gtaaggcagg	cacctggaca	gggtctggaa	900
tggattggat	acattaatcc	tagccgtggt	tataactaatt	acaatcagaa	gttcaaggac	960
cgcgtcacaa	tcactacaga	caaatccacc	agcacagcct	acatggaact	gagcagcctg	1020
cgttctgagg	acactgcagt	ctattactgt	gcaagatatt	atgatgatca	ttactgcctt	1080
gactactggg	gccaaggcac	cacggtcacc	gtctcctcag	gcgaaggtag	tagtactggt	1140
tctggtggaa	gtggaggttc	aggtggagca	gacgacattg	tactgaccca	gtctccagca	1200
actctgtctc	tgtctccagg	ggagcgtgcc	accctgagct	gcagagccag	tcaaagtgtg	1260
agttacatga	actggtacca	gcagaagccg	ggcaaggcac	ccaaaagatg	gatttatgac	1320
acatccaaag	tggcttctgg	agtccctgct	cgcttcagtg	gcagtgggtc	tgggaccgac	1380

tactctctca caatcaacag cttggaggct gaagatgctg ccacttatta ctgccaacag 1440

tggagtagta acccgctcac gttcgggtggc gggaccaagg tggagatcaa a 1491

<210> 269

<211> 497

<212> PRT

<213> artificial sequence

<220>

<223> 5-10/VH7VL2 HLHL

<400> 269

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
1 5 10 15

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
20 25 30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
35 40 45

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
65 70 75 80

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
85 90 95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser
130 135 140

Ser Leu Thr Val Thr Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser
145 150 155 160

Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu Thr Trp
165 170 175

Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala
180 185 190

Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser
195 200 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu
210 215 220

Ala Val Tyr Tyr Cys Gln Asn Asp Tyr Ser Tyr Pro Leu Thr Phe Gly
225 230 235 240

Ala Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Asp Val
245 250 255

Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val
260 265 270

Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met
275 280 285

His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr
290 295 300

Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp
305 310 315 320

Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu
325 330 335

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
340 345 350

Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr
355 360 365

Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser
370 375 380

Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser Pro Ala
385 390 395 400

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
405 410 415

Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys
 420 425 430

Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val
 435 440 445

Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr
 450 455 460

Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
 465 470 475 480

Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
 485 490 495

Lys

<210> 270
 <211> 1488
 <212> DNA
 <213> artificial sequence

<220>
 <223> 5-10/VL2VH7 LHLH

<400> 270
 gagctcgtga tgacacagtc tccatcctcc ctgactgtga cagcaggaga gaaggtcact 60
 atgagctgca agtccagtca gagtctgtta aacagtggaa atcaaaagaa ctacttgacc 120
 tgggtaccagc agaaaccagg gcagcctcct aaactgttga tctactgggc atccactagg 180
 gaatctgggg tccctgatcg cttcacaggc agtggatctg gaacagattt cactctcacc 240
 atcagcagtg tgcaggctga agacctggca gtttattact gtcagaatga ttatagttat 300
 ccgctcacgt tcggtgctgg gaccaagctt gagatcaaag gtggtggtgg ttctggcggc 360
 ggcggctccg gtggtggtgg ttctgaggtg cagctgctcg agcagtctgg agctgagctg 420
 gtaaggcctg ggacttcagt gaagatatcc tgcaaggctt ctggatacgc cttcactaac 480
 tactggctag gttgggtaaa gcagaggcct ggacatggac ttgagtggat tggagatatt 540
 ttccctggaa gtggtaatat ccactacaat gagaagttca agggcaaagc cacactgact 600
 gcagacaaat cttcgagcac agcctatatg cagctcagta gcctgacatt tgaggactct 660
 gctgtctatt tctgtgcaag actgaggaac tgggacgagc ctatggacta ctggggccaa 720

gggaccacgg tcaccgtctc ctccggaggt ggtggatccg acattgtact gacccagtct 780
ccagcaactc tgtctctgtc tccaggggag cgtgccaccc tgagctgcag agccagtcaa 840
agtgttaagt acatgaactg gtaccagcag aagccgggca aggcacccaa aagatggatt 900
tatgacacat ccaaagtggc ttctggagtc cctgctcgct tcagtggcag tgggtctggg 960
accgactact ctctcacaat caacagcttg gaggtgaag atgctgccac ttattactgc 1020
caacagtgga gtagtaacct gctcacgttc ggtggcgagg ccaaggtgga gatcaaaggc 1080
gaaggtaact gtactgggtc tgggtggaagt ggaggttcag gtggagcaga cgacgtccaa 1140
ctggtgcagt caggggctga agtgaaaaaa cctggggcct cagtgaagggt gtcctgcaag 1200
gcttctggct acacctttac taggtacacg atgcactggg taaggcaggc acctggacag 1260
ggtctggaat ggattggata cattaatcct agccgtgggt atactaatta caatcagaag 1320
ttcaaggacc gcgtcacaat cactacagac aaatccacca gcacagccta catggaactg 1380
agcagcctgc gttctgagga cactgcagtc tattactgtg caagatatta tgatgatcat 1440
tactgccttg actactgggg ccaaggcacc acggtcaccg tctcctca 1488

<210> 271

<211> 496

<212> PRT

<213> artificial sequence

<220>

<223> 5-10/VL2VH7 LHLH

<400> 271

Glu Leu Val Met Thr Gln Ser Pro Ser Ser Leu Thr Val Thr Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Asp Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile
100 105 110

Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
130 135 140

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
145 150 155 160

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
165 170 175

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
180 185 190

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
195 200 205

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
210 215 220

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
225 230 235 240

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Val
245 250 255

Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
260 265 270

Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr
275 280 285

Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser
290 295 300

Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
305 310 315 320

Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala

325

330

335

Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly
 340 345 350

Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr Gly Ser Gly
 355 360 365

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu Val Gln Ser
 370 375 380

Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys
 385 390 395 400

Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln
 405 410 415

Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg
 420 425 430

Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr
 435 440 445

Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg
 450 455 460

Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His
 465 470 475 480

Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 485 490 495

<210> 272

<211> 1491

<212> DNA

<213> artificial sequence

<220>

<223> 5-10/VL2VH7 HLLH

<400> 272

gaggtgcagc tgctcgagca gtctggagct gagctggtaa ggcctgggac ttcagtgaag 60

atatactgca aggcttctgg atacgccttc actaactact ggctagggttg ggtaaagcag 120

aggcctggac atggacttga gtggattgga gatattttcc ctggaagtgg taatatccac 180

tacaatgaga agttcaaggg caaagccaca ctgactgcag acaaattctc gagcacagcc 240

tatatgcagc tcagtagcct gacatttgag gactctgctg tctatttctg tgcaagactg 300
aggaactggg acgagcctat ggactactgg ggccaaggga ccacggtcac cgtctcctca 360
ggtggtggtg gttctggcgg cggcggctcc ggtggtggtg gttctgagct cgtgatgaca 420
cagtctccat cctccctgac tgtgacagca ggagagaagg tcactatgag ctgcaagtcc 480
agtcagagtc tgttaaacag tggaaatcaa aagaactact tgacctggtg ccagcagaaa 540
ccagggcagc ctctaaact gttgatctac tgggcatcca ctagggaatc tggggtcctt 600
gatcgcttca caggcagtgg atctggaaca gatttcactc tcaccatcag cagtgtgcag 660
gctgaagacc tggcagttta ttactgtcag aatgattata gttatccgct cacgttcggt 720
gctgggacca agcttgagat caaatccgga ggtggtggat ccgacattgt actgaccag 780
tctccagcaa ctctgtctct gtctccaggg gagcgtgcc aacctgagctg cagagccagt 840
caaagtgtaa gttacatgaa ctggtaccag cagaagccgg gcaaggcacc caaaagatgg 900
atztatgaca catccaaagt ggcttctgga gtccctgctc gcttcagtgg cagtgggtct 960
gggaccgact actctctcac aatcaacagc ttggaggctg aagatgctgc cacttattac 1020
tgccaacagt ggagtagtaa cccgctcacg ttcggtggcg ggaccaaggt ggagatcaaa 1080
ggcgaaggta ctagtactgg ttctggtgga agtggagggt cagggtggagc agacgacgtc 1140
caactggtgc agtcaggggc tgaagtgaaa aaacctgggg cctcagtgaa ggtgtcctgc 1200
aaggcttctg gctacacctt tactaggtac acgatgcact gggtaaggca ggcacctgga 1260
cagggtctgg aatggattgg atacattaat cctagccgtg gttatactaa ttacaatcag 1320
aagttcaagg accgcgtcac aatcactaca gacaaatcca ccagcacagc ctacatggaa 1380
ctgagcagcc tgcgttctga ggacactgca gtctattact gtgcaagata ttatgatgat 1440
cattactgcc ttgactactg gggccaaggc accacggtca ccgtctctc a 1491

<210> 273
<211> 497
<212> PRT
<213> artificial sequence

<220>
<223> 5-10/VL2VH7 HLLH

<400> 273

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
1 5 10 15

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn

20

25

30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
 35 40 45

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
 50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
 65 70 75 80

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
 85 90 95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser
 130 135 140

Ser Leu Thr Val Thr Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser
 145 150 155 160

Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu Thr Trp
 165 170 175

Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala
 180 185 190

Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser
 195 200 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu
 210 215 220

Ala Val Tyr Tyr Cys Gln Asn Asp Tyr Ser Tyr Pro Leu Thr Phe Gly
 225 230 235 240

Ala Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Asp Ile
 245 250 255

Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg
260 265 270

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp
275 280 285

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr
290 295 300

Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser
305 310 315 320

Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala
325 330 335

Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly
340 345 350

Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr Gly Ser
355 360 365

Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu Val Gln
370 375 380

Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys
385 390 395 400

Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg
405 410 415

Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser
420 425 430

Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile
435 440 445

Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu
450 455 460

Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp
465 470 475 480

His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser
485 490 495

Ser

<210> 274
<211> 1488
<212> DNA
<213> artificial sequence

<220>
<223> 5-10/VH7VL3 LHHL

<400> 274
gagctcgtga tgacacagtc tccatcctcc ctgactgtga cagcaggaga gaaggtcact 60
atgagctgca agtccagtca gagtctgtta aacagtggaa atcaaaagaa ctacttgacc 120
tggtaccagc agaaaccagg gcagcctcct aaactgttga tctactgggc atccactagg 180
gaatctgggg tcctgatcg cttcacaggc agtggatctg gaacagattt cactctcacc 240
atcagcagtg tgcaggctga agacctggca gtttattact gtcagaatga ttatagttat 300
ccgctcacgt tcggtgctgg gaccaagctt gagatcaaag gtggtggtgg ttctggcggc 360
ggcggctccg gtggtggtgg ttctgaggtg cagctgctcg agcagtctgg agctgagctg 420
gtaaggcctg ggacttcagt gaagatatcc tgcaaggctt ctggatacgc cttcactaac 480
tactggctag gttgggtaaa gcagaggcct ggacatggac ttgagtggat tggagatatt 540
ttccctggaa gtggtaatat ccactacaat gagaagttca agggcaaagc cacactgact 600
gcagacaaat cttcgagcac agcctatatg cagctcagta gcctgacatt tgaggactct 660
gctgtctatt tctgtgcaag actgaggaac tgggacgagc ctatggacta ctggggccaa 720
gggaccacgg tcaccgtctc ctccggaggt ggtggatccg acgtccaact ggtgcagtca 780
ggggctgaag tgaaaaaacc tggggcctca gtgaagggtg cctgcaaggc ttctggctac 840
acctttacta ggtacacgat gcaactgggtta aggcaggcac ctggacaggg tctggaatgg 900
attggataca ttaatcctag ccgtggttat actaattaca atcagaagtt caaggaccgc 960
gtcacaatca ctacagacaa atccaccagc acagcctaca tggaactgag cagcctgcgt 1020
tctgaggaca ctgcagtcta ttactgtgca agatattatg atgatcatta ctgccttgac 1080
tactggggcc aaggcaccac ggtcaccgtc tectcaggcg aaggtagtag tactggttct 1140
ggtggaagtg gaggttcagg tggagcagac gacattgtac tgaccacgac tccagcaact 1200
ctgtctctgt ctccagggga gcgtgccacc ctgacctgca gagccagttc aagtgttaagt 1260
tacatgaact ggtaccagca gaagccgggc aaggcaccca aaagatggat ttatgacaca 1320
tccaaagtgg cttctggagt cctgctcgc ttcaagtggca gtgggtctgg gaccgactac 1380

tctctcacaa tcaacagctt ggaggctgaa gatgctgcca cttattactg ccaacagtgg 1440

agtagtaacc cgctcacgtt cggtggcggg accaaggtgg agatcaaa 1488

<210> 275

<211> 496

<212> PRT

<213> artificial sequence

<220>

<223> 5-10/VH7VL3 LHHL

<400> 275

Glu Leu Val Met Thr Gln Ser Pro Ser Ser Leu Thr Val Thr Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Asp Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile
100 105 110

Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
130 135 140

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
145 150 155 160

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
165 170 175

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
 180 185 190

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
 195 200 205

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
 210 215 220

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
 225 230 235 240

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Val Gln
 245 250 255

Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys
 260 265 270

Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His
 275 280 285

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile
 290 295 300

Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg
 305 310 315 320

Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu
 325 330 335

Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr
 340 345 350

Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val
 355 360 365

Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser Gly
 370 375 380

Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser Pro Ala Thr
 385 390 395 400

Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys Arg Ala Ser
 405 410 415

Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
 420 425 430

Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro
 435 440 445

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
 450 455 460

Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 465 470 475 480

Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 485 490 495

<210> 276

<211> 1491

<212> DNA

<213> artificial sequence

<220>

<223> 5-10/VH7VL3 HLHL

<400> 276

gaggtgcagc tgctcgagca gtctggagct gagctggtaa ggcctgggac ttcagtgaag	60
atatactgca aggccttctgg atacgccttc actaactact ggctagggttg ggtaaagcag	120
aggcctggac atggacttga gtggattgga gatattttcc ctggaagtgg taatatccac	180
tacaatgaga agttcaaggg caaagccaca ctgactgcag acaaattctc gagcacagcc	240
tatatgcagc tcagtagcct gacatttgag gactctgctg tctattttctg tgcaagactg	300
aggaactggg acgagcctat ggactactgg ggccaaggga ccacggtcac cgtctcctca	360
ggtggtggtg gttctggcgg cggcggctcc ggtggtggtg gttctgagct cgtgatgaca	420
cagtctccat cctccctgac tgtgacagca ggagagaagg tcactatgag ctgcaagtcc	480
agtcagagtc tgtaaagcag tggaatatcaa aagaactact tgacctggtg ccagcagaaa	540
ccagggcagc ctctaaact gttgatctac tgggcatcca ctagggaatc tggggtcctt	600
gatcgcttca caggcagtgg atctggaaca gatttcactc tcaccatcag cagtgtgcag	660
gctgaagacc tggcagttta ttactgtcag aatgattata gttatccgct cacgttcggt	720
gctgggacca agcttgagat caaatccgga ggtggtggat ccgacgtcca actggtgcag	780
tcaggggctg aagtgaaaaa acctggggcc tcagtgaagg tgtcctgcaa ggcttctggc	840

tacaccttta ctaggtacac gatgcactgg gtaaggcagg cacctggaca gggctctggaa 900
tggattggat acattaatcc tagccgtggg tataactaatt acaatcagaa gttcaaggac 960
cgcgtcacaa tcactacaga caaatccacc agcacagcct acatggaact gagcagcctg 1020
cggtctgagg aactgcagt ctattactgt gcaagatatt atgatgatca ttactgcctt 1080
gactactggg gccaaaggcac cacggtcacc gtctcctcag gcgaaggtag tagtactggg 1140
tctgggtggaa gtggagggttc aggtggagca gacgacattg tactgaccca gtctccagca 1200
actctgtctc tgtctccagg ggagcgtgcc accctgacct gcagagccag ttcaagtgtg 1260
agttacatga actggtacca gcagaagccg ggcaaggcac ccaaaagatg gatttatgac 1320
acatccaaag tggcttctgg agtccttgct cgcttcagtg gcagtgggtc tgggaccgac 1380
tactctctca caatcaacag cttggagggt gaagatgctg ccacttatta ctgccaacag 1440
tggagtagta acccgctcac gttcggtggc gggaccaagg tggagatcaa a 1491

<210> 277
<211> 497
<212> PRT
<213> artificial sequence

<220>
<223> 5-10/VH7VL3 HLHL

<400> 277

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
1 5 10 15

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
20 25 30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
35 40 45

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
65 70 75 80

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
85 90 95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser
130 135 140

Ser Leu Thr Val Thr Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser
145 150 155 160

Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu Thr Trp
165 170 175

Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala
180 185 190

Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser
195 200 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu
210 215 220

Ala Val Tyr Tyr Cys Gln Asn Asp Tyr Ser Tyr Pro Leu Thr Phe Gly
225 230 235 240

Ala Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Asp Val
245 250 255

Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val
260 265 270

Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met
275 280 285

His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr
290 295 300

Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp
305 310 315 320

Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu
325 330 335

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg

340345350

Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr
355360365

Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser
370375380

Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser Pro Ala
385390395400

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys Arg Ala
405410415

Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys
420425430

Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val
435440445

Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr
450455460

Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
465470475480

Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
485490495

Lys

<210> 278
<211> 1488
<212> DNA
<213> artificial sequence

<220>
<223> 5-10/VL3VH7 LHLH

<400> 278
gagctcgtga tgacacagtc tccatcctcc ctgactgtga cagcaggaga gaaggtcact 60
atgagctgca agtcacgtca gagtctgtta aacagtggaa atcaaaagaa ctacttgacc 120
tggtaccagc agaaaccagg gcagcctcct aaactgttga tctactgggc atccactagg 180
gaatctgggg tccctgatcg cttcacaggc agtggatctg gaacagattt cactctcacc 240

atcagcagtg tgcaggctga agacctggca gtttattact gtcagaatga ttatagttat 300
ccgctcacgt tcggtgctgg gaccaagctt gagatcaaag gtggtggtgg ttctggcggc 360
ggcggctccg gtggtggtgg ttctgaggtg cagctgctcg agcagtctgg agctgagctg 420
gtaaggcctg ggacttcagt gaagatatcc tgcaaggctt ctggatacgc cttcactaac 480
tactggctag gttgggtaaa gcagaggcct ggacatggac ttgagtggat tggagatatt 540
ttccctggaa gtggtaatat ccactacaat gagaagttca agggcaaagc cacactgact 600
gcagacaaat cttcgagcac agcctatatg cagctcagta gcctgacatt tgaggactct 660
gctgtctatt tctgtgcaag actgaggaac tgggacgagc ctatggacta ctggggccaa 720
gggaccacgg tcaccgtctc ctccggaggt ggtggatccg acattgtact gacccagtct 780
ccagcaactc tgtctctgtc tccaggggag cgtgccaccc tgacctgcag agccagttca 840
agtgtaagtt acatgaactg gtaccagcag aagccgggca aggcacccaa aagatggatt 900
tatgacacat ccaaagtggc ttctggagtc cctgctcgct tcagtggcag tgggtctggg 960
accgactact ctctcacaat caacagcttg gaggtgaag atgctgccac ttattactgc 1020
caacagtgga gtagtaaccc gctcacgttc ggtggcgagg ccaaggtgga gatcaaaggc 1080
gaaggacta gtactgggtc tgggtggaagt ggaggttcag gtggagcaga cgacgtccaa 1140
ctggtgcagt caggggctga agtgaaaaaa cctggggcct cagtgaaggt gtcctgcaag 1200
gcttctggct acacctttac taggtacacg atgcactggg taaggcaggc acctggacag 1260
ggtctggaat ggattggata cattaatcct agccgtgggt atactaatta caatcagaag 1320
ttcaaggacc gcgtcacaat cactacagac aaatccacca gcacagccta catggaactg 1380
agcagcctgc gttctgagga cactgcagtc tattactgtg caagatatta tgatgatcat 1440
tactgccttg actactgggg ccaaggcacc acggtcaccg tctcctca 1488

<210> 279

<211> 496

<212> PRT

<213> artificial sequence

<220>

<223> 5-10/VL3VH7 LHLH

<400> 279

Glu Leu Val Met Thr Gln Ser Pro Ser Ser Leu Thr Val Thr Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
130 135 140

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
145 150 155 160

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
165 170 175

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
180 185 190

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
195 200 205

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
210 215 220

Cys Ala. Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
225 230 235 240

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Val
245 250 255

Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
 260 265 270

Thr Leu Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr
 275 280 285

Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser
 290 295 300

Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
 305 310 315 320

Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala
 325 330 335

Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly
 340 345 350

Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr Gly Ser Gly
 355 360 365

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu Val Gln Ser
 370 375 380

Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys
 385 390 395 400

Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln
 405 410 415

Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg
 420 425 430

Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr
 435 440 445

Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg
 450 455 460

Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His
 465 470 475 480

Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 485 490 495

<210> 280
<211> 1491
<212> DNA
<213> artificial sequence

<220>
<223> 5-10/VL3VH7 HLLH

<400> 280
gaggtgcagc tgctcgagca gtctggagct gagctggtaa ggcctgggac ttcagtgaag 60
atatcctgca aggcttctgg atacgccttc actaactact ggctaggttg ggtaaagcag 120
aggcctggac atggacttga gtggattgga gatattttcc ctggaagtgg taatatccac 180
tacaatgaga agttcaaggg caaagccaca ctgactgcag acaaatcttc gagcacagcc 240
tatatgcagc tcagtagcct gacatttgag gactctgctg tctatttctg tgcaagactg 300
aggaaactggg acgagcctat ggactactgg ggccaaggga ccacggtcac cgtctcctca 360
ggtggtggtg gttctggcgg cggcggctcc ggtggtggtg gttctgagct cgtgatgaca 420
cagtctccat cctccctgac tgtgacagca ggagagaagg tcactatgag ctgcaagtcc 480
agtcagagtc tgtaaacag tggaaatcaa aagaactact tgacctggta ccagcagaaa 540
ccagggcagc ctctaaact gttgatctac tgggcatcca ctagggaatc tggggtcctt 600
gatcgcttca caggcagtgg atctggaaca gatttcactc tcaccatcag cagtgtgcag 660
gctgaagacc tggcagttta ttactgtcag aatgattata gttatccgct cacgttcggt 720
gctgggacca agcttgagat caaatccgga ggtggtggat ccgacattgt actgaccag 780
tctccagcaa ctctgtctct gtctccaggg gagcgtgcc aacctgacctg cagagccagt 840
tcaagtgtaa gttacatgaa ctggtaccag cagaagccgg gcaaggcacc caaaagatgg 900
atztatgaca catcaaagt ggcttctgga gtccctgctc gcttcagtgg cagtgggtct 960
gggaccgact actctctcac aatcaacagc ttggaggctg aagatgctgc cacttattac 1020
tgccaacagt ggagtagtaa cccgctcacg ttcggtggcg ggaccaaggt ggagatcaaa 1080
ggcgaaggta ctagtactgg ttctggtgga agtggaggtt caggtggagc agacgacgtc 1140
caactggtgc agtcaggggc tgaagtgaaa aaacctgggg cctcagtgaa ggtgtcctgc 1200
aaggcttctg gctacacctt tactaggtac acgatgcact gggtaaggca ggcacctgga 1260
cagggctctgg aatggattgg atacattaat cctagccgtg gttatactaa ttacaatcag 1320
aagttcaagg accgcgtcac aatcactaca gacaaatcca ccagcacagc ctacatggaa 1380
ctgagcagcc tgcgttctga ggacactgca gtctattact gtgcaagata ttatgatgat 1440
cattactgcc ttgactactg gggccaaggc accacgggtca ccgtctcctc a 1491

<210> 281
<211> 497
<212> PRT
<213> artificial sequence

<220>
<223> 5-10/VL3VH7 HLLH

<400> 281

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
1 5 10 15

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
20 25 30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
35 40 45

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
65 70 75 80

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
85 90 95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser
130 135 140

Ser Leu Thr Val Thr Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser
145 150 155 160

Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu Thr Trp
165 170 175

Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala
180 185 190

Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser
195 200 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu
210 215 220

Ala Val Tyr Tyr Cys Gln Asn Asp Tyr Ser Tyr Pro Leu Thr Phe Gly
225 230 235 240

Ala Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Asp Ile
245 250 255

Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg
260 265 270

Ala Thr Leu Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp
275 280 285

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr
290 295 300

Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser
305 310 315 320

Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala
325 330 335

Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly
340 345 350

Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr Gly Ser
355 360 365

Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu Val Gln
370 375 380

Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys
385 390 395 400

Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg
405 410 415

Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser
420 425 430

Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile
435 440 445

Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu
450 455 460

Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp
465 470 475 480

His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser
485 490 495

Ser

<210> 282
<211> 1497
<212> DNA
<213> artificial sequence

<220>
<223> VL1/VH5x4-7 LHHL

<400> 282
gacattcaga tgaccagtc tccatctagc ctgtctgcat ctgtcgggga ccgtgtcacc 60
atcacctgca gagccagtca aagtgttaagt tacatgaact ggtaccagca gaagccgggc 120
aaggcaccca aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctcgc 180
ttcagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa 240
gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cggtggcggg 300
accaaggtgg agatcaaagg cgaaggtact agtactgggt ctgggtggaag tggaggttca 360
gggtggagcag acgacgtcca actgggtgcag tcaggggctg aagtgaaaaa acctggggcc 420
tcagtgaagg tgtcctgcaa ggcttctggc tacaccttta ctaggtacac gatgcactgg 480
gtaaggcagg cacctggaca gggctctggaa tggattggat acattaatcc tagccgtggg 540
tatactaatt acgcagacag cgtcaagggc cgcttcacia tcactacaga caaatccacc 600
agcacagcct acatggaact gagcagcctg cgttctgagg aactgcaac ctattactgt 660
gcaagatatt atgatgatca ttactgcctt gactactggg gccaaaggcac cacggtcacc 720
gtctcctccg gaggtgggtg atccgaggtg cagctgctcg agcagtctgg agctgagctg 780
gcgaggcctg gggcttcagt gaagctgtcc tgcaaggctt ctggctacac cttcaciaaac 840

tatgggtttaa gctgggtgaa gcagaggcct ggacagggtcc ttgagtggat tggagagggt 900
 taccctagaa ttggtaatgc ttactacaat gagaagttca agggcaaggc cacactgact 960
 gcagacaaat cctccagcac agcgtccatg gagctccgca gcctgacctc tgaggactct 1020
 gcggtctatt tctgtgcaag acgggggatcc tacgatacta actacgactg gtacttcgat 1080
 gtctgggggcc aagggaaccac ggtcaccgtc tcctcagggtg gtggtgggttc tggcggcggc 1140
 ggctccgggtg gtggtgggttc tgagctcgtg atgaccaga ctccactctc cctgcctgtc 1200
 agtcttggag atcaagcctc catctcttgc agatctagtc agagccttgt acacagtaat 1260
 ggaaacacct atttacattg gtacctgcag aagccaggcc agtctccaaa gctcctgatc 1320
 tacaaagttt ccaaccgatt ttctggggtc ccagacaggt tcagtggcag tggatcaggg 1380
 acagatttca cactcaagat cagcagagtg gaggtgagg atctgggagt ttatttctgc 1440
 tctcaaagta cacatgttcc gtacacgttc ggagggggga ccaagcttga gatcaaa 1497

<210> 283
 <211> 499
 <212> PRT
 <213> artificial sequence

<220>
 <223> VL1/VH5x4-7 LHHL

<400> 283

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
 20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
 35 40 45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
 85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
 100 105 110

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
115 120 125

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
145 150 155 160

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
165 170 175

Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe
180 185 190

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
195 200 205

Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr
210 215 220

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
225 230 235 240

Val Ser Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln Ser
245 250 255

Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys Lys
260 265 270

Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys Gln
275 280 285

Arg Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg Ile
290 295 300

Gly Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr
305 310 315 320

Ala Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr
325 330 335

Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr Asp

340

345

350

Thr Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val
 355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 370 375 380

Gly Gly Ser Glu Leu Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val
 385 390 395 400

Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu
 405 410 415

Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro
 420 425 430

Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
 435 440 445

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 450 455 460

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys
 465 470 475 480

Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu
 485 490 495

Glu Ile Lys

<210> 284

<211> 1500

<212> DNA

<213> artificial sequence

<220>

<223> VH5/VL1x4-7 HLHL

<400> 284

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cctggacagg gtctggaatg gattggatac attaataccta gccgtgggta tactaattac 180

gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 240

atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300
 gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctccctcagge 360
 gaagg tacta gtactgggtt tggtggaagt ggagggttcag gtggagcaga cgacattcag 420
 atgacccagt ctccatctag cctgtctgca tctgtcgggg accgtgtcac catcacctgc 480
 agagccagtc aaagtgt aag ttacatgaac tggtaccagc agaagccggg caaggcaccc 540
 aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
 agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
 acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaagggtg 720
 gagatcaaat ccggagggtg tggatccgag gtgcagctgc tcgagcagtc tggagctgag 780
 ctggcgaggc ctggggcttc agtgaagctg tcctgcaagg cttctggcta caccttcaca 840
 aactatgggt taagctgggt gaagcagagg cctggacagg tccttgagtg gattggagag 900
 gtttatecta gaattggtaa tgcttactac aatgagaagt tcaagggcaa ggccacactg 960
 actgcagaca aatcctccag cacagcgtcc atggagctcc gcagcctgac ctctgaggac 1020
 tctgcggtct atttctgtgc aagacgggga tcctacgata ctaactacga ctggtacttc 1080
 gatgtctggg gccaaaggac cacggtcacc gtctcctcag gtggtggtgg ttctggcggc 1140
 ggcggctccg gtggtggtgg ttctgagctc gtgatgacct agactccact ctccctgcct 1200
 gtcagtcttg gagatcaagc ctccatctct tgcagatcta gtcagagcct tgtacacagt 1260
 aatggaaaca cctatttaca ttggtacctg cagaagccag gccagtctcc aaagctcctg 1320
 atctacaaag tttccaaccg attttctggg gtcccagaca ggttcagtgg cagtggatca 1380
 gggacagatt tcacactcaa gatcagcaga gtggaggctg aggatctggg agtttatttc 1440
 tgctctcaaa gtacacatgt tccgtacacg ttcggagggg ggaccaagct tgagatcaaa 1500

<210> 285
 <211> 500
 <212> PRT
 <213> artificial sequence

<220>
 <223> VH5/VL1x4-7 HLHL

<400> 285

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr

20

25

30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
 85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
 115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser
 130 135 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
 145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln
 245 250 255

Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys
260 265 270

Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys
275 280 285

Gln Arg Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg
290 295 300

Ile Gly Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu
305 310 315 320

Thr Ala Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu
325 330 335

Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr
340 345 350

Asp Thr Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr
355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
370 375 380

Gly Gly Gly Ser Glu Leu Val Met Thr Gln Thr Pro Leu Ser Leu Pro
385 390 395 400

Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
405 410 415

Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys
420 425 430

Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe
435 440 445

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
450 455 460

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe
465 470 475 480

Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys
485 490 495

Leu Glu Ile Lys
500

<210> 286
<211> 1497
<212> DNA
<213> artificial sequence

<220>
<223> VL1/VH5x4-7 LHLH

<400> 286
gacattcaga tgacccagtc tccatctagc ctgtctgcat ctgtcgggga ccgtgtcacc 60
atcacctgca gagccagtca aagtgttaagt tacatgaact ggtaccagca gaagccgggc 120
aaggcaccga aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctcgc 180
ttcagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa 240
gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cgggtggcggg 300
accaaggtgg agatcaaagg cgaaggtact agtactgggt ctggtggaag tggaggttca 360
gggtggagcag acgacgtcca actgggtgcag tcaggggctg aagtgaaaaa acctggggcc 420
tcagtgaagg tgtcctgcaa ggcttctggc tacaccttta ctaggtacac gatgcactgg 480
gtaaggcagg cacctggaca gggctctggaa tggattggat acattaatcc tagccgtggg 540
tatactaatt acgcagacag cgtcaagggc cgcttcacia tcactacaga caaatccacc 600
agcacagcct acatggaact gagcagcctg cgcttctgagg aactgcaac ctattactgt 660
gcaagatatt atgatgatca ttactgcctt gactactggg gccaaaggcac cacggtcacc 720
gtctcctccg gaggtgggtg atccgagctc gtgatgaccc agactccact ctccctgcct 780
gtcagtcttg gagatcaagc ctccatctct tgcagatcta gtcagagcct tgtacacagt 840
aatggaaaca cctatttaca ttggtacctg cagaagccag gccagtctcc aaagctcctg 900
atctacaaag ttccaaccg attttctggg gtcccagaca gggtcagtgg cagtggatca 960
gggacagatt tcacactcaa gatcagcaga gtggaggctg aggatctggg agtttatttc 1020
tgctctcaaa gtacacatgt tccgtacacg ttcggagggg ggaccaagct tgagatcaaa 1080
gggtggtggtg gttctggcgg cggcggctcc ggtggtggtg gttctgaggt gcagctgctc 1140
gagcagtctg gagctgagct ggcgaggcct ggggcttcag tgaagctgtc ctgcaaggct 1200
tctggctaca ccttcacaaa ctatggttta agctgggtga agcagaggcc tggacaggctc 1260
cttgagtgga ttggagaggt ttatcctaga attggtaatg ctactacaa tgagaagttc 1320
aagggcaagg ccacactgac tgcagacaaa tcctccagca cagcgtccat ggagctccgc 1380

agcctgacct ctgaggactc tgcggtctat ttctgtgcaa gacggggatc ctacgatact 1440

aactacgact ggtacttcga tgtctggggc caagggacca cggtcaccgt ctcctca 1497

<210> 287

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> VL1/VH5x4-7 LHLH

<400> 287

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
100 105 110

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
115 120 125

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
145 150 155 160

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
165 170 175

Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe
180 185 190

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
195 200 205

Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr
210 215 220

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
225 230 235 240

Val Ser Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Thr Pro
245 250 255

Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg
260 265 270

Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp
275 280 285

Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val
290 295 300

Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser
305 310 315 320

Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu
325 330 335

Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly
340 345 350

Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly
355 360 365

Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln Ser Gly
370 375 380

Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala
385 390 395 400

Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys Gln Arg
405 410 415

Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg Ile Gly
420 425 430

Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala
435 440 445

Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr Ser
450 455 460

Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr Asp Thr
465 470 475 480

Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val Thr
485 490 495

Val Ser Ser

<210> 288

<211> 1500

<212> DNA

<213> artificial sequence

<220>

<223> VH5/VL1x4-7 HLLH

<400> 288

gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctgggggcctc agtgaagggtg 60

tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 120

cctggacagg gtctggaatg gattggatac attaataccta gccgtgggtta tactaattac 180

gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 240

atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300

gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc 360

gaaggacta gtactgggtc tgggtggaagt ggagggttcag gtggagcaga cgacattcag 420

atgaccagtc ctccatctag cctgtctgca tctgtcgggg accgtgtcac catcacctgc 480

agagccagtc aaagtgtaag ttacatgaac tgggtaccagc agaagccggg caaggcaccc 540

aaaagatgga ttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600

agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660

acttattact gccaacagtg gagtagtaac ccgctcacgt tcgggtggcgg gaccaagggtg 720

gagatcaaat ccggaggtgg tggatccgag ctcgtgatga cccagactcc actctccctg 780
cctgtcagtc ttggagatca agcctccatc tcttgcagat ctagtcagag ccttgtacac 840
agtaatggaa acacctatctt acattggtac ctgcagaagc caggccagtc tccaaagctc 900
ctgatctaca aagtttccaa ccgattttct ggggtcccag acaggttcag tggcagtgga 960
tcagggacag atttcacact caagatcagc agagtggagg ctgaggatct gggagtattat 1020
ttctgctctc aaagtacaca tgttccgtac acgttcggag gggggaccaa gcttgagatc 1080
aaaggtggtg gtggttctgg cggcggcggc tccggtggtg gtggttctga ggtgcagctg 1140
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gcttctggct acaccttcac aaactatggt ttaagctggg tgaagcagag gcctggacag 1260
gtccttgagt ggattggaga ggtttatcct agaattggtg atgcttacta caatgagaag 1320
ttcaagggca aggccacact gactgcagac aaatcctcca gcacagcgtc catggagctc 1380
cgcagcctga cctctgagga ctctgcggtc tatttctgtg caagacgggg atcctacgat 1440
actaactacg actggtactt cgatgtctgg ggccaaggga ccacggtcac cgtctcctca 1500

<210> 289
<211> 500
<212> PRT
<213> artificial sequence

<220>
<223> VH5/VL1x4-7 HLLH

<400> 289

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser
130 135 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Thr
245 250 255

Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys
260 265 270

Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His
275 280 285

Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys
290 295 300

Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
305 310 315 320

Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp

325

330

335

Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe
 340 345 350

Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly
 355 360 365

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln Ser
 370 375 380

Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys Lys
 385 390 395 400

Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys Gln
 405 410 415

Arg Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg Ile
 420 425 430

Gly Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr
 435 440 445

Ala Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr
 450 455 460

Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr Asp
 465 470 475 480

Thr Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val
 485 490 495

Thr Val Ser Ser
 500

<210> 290
 <211> 1497
 <212> DNA
 <213> artificial sequence

<220>
 <223> VL2/VH5x4-7 LHHL

<400> 290
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 ctgagctgca gagccagtc aagtgttaagt tacatgaact ggtaccagca gaagccgggc 120

aaggcacca aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctcgc 180
ttcagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa 240
gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cggtggcggg 300
accaaggtgg agatcaaagg cgaaggtact agtactgggt ctggtggaag tggaggttca 360
ggtggagcag acgacgtcca actggtgcag tcaggggctg aagtgaaaaa acctggggcc 420
tcagtgaagg tgtcctgcaa ggcttctggc tacaccttta ctaggtacac gatgcactgg 480
gtaaggcagg cacctggaca gggctctggaa tggattggat acattaatcc tagccgtggt 540
tatactaatt acgcagacag cgtcaagggc cgcttcacia tcactacaga caaatccacc 600
agcacagcct acatggaact gagcagcctg cgttctgagg aactgcaac ctattactgt 660
gcaagatatt atgatgatca ttactgcctt gactactggg gccaaaggcac cacggtcacc 720
gtctcctccg gaggtgggtg atccgaggtg cagctgctcg agcagtctgg agctgagctg 780
gcgaggcctg gggcttcagt gaagctgtcc tgcaaggctt ctggctacac cttcaciaaac 840
tatggtttaa gctgggtgaa gcagaggcct ggacaggctc ttgagtggat tggagaggtt 900
tatectagaa ttggtaatgc ttactacaat gagaagttca agggcaaggc cacactgact 960
gcagacaaat cctccagcac agcgtccatg gagctccgca gcctgacctc tgaggactct 1020
gcggtctatt tctgtgcaag acggggatcc tacgatacta actacgactg gtacttcgat 1080
gtctggggcc aagggaccac ggtcaccgtc tcctcaggtg gtggtggttc tggcggcggc 1140
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agtcttggag atcaagctc catctcttgc agatctagtc agagccttgt acacagtaat 1260
ggaaacacct atttacattg gtacctgcag aagccaggcc agtctccaaa gctcctgatc 1320
tacaaagttt ccaaccgatt ttctggggtc ccagacaggt tcagtggcag tggatcaggg 1380
acagatttca cactcaagat cagcagagtg gaggctgagg atctgggagt ttatttctgc 1440
tctcaaagta cacatgttcc gtacacgttc ggagggggga ccaagcttga gatcaaa 1497

<210> 291

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> VL2/VH5x4-7 LHL

<400> 291

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly

1		5		10		15									
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Ser	Tyr	Met
		20						25					30		
Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Arg	Trp	Ile	Tyr
		35					40					45			
Asp	Thr	Ser	Lys	Val	Ala	Ser	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser
	50					55					60				
Gly	Ser	Gly	Thr	Asp	Tyr	Ser	Leu	Thr	Ile	Asn	Ser	Leu	Glu	Ala	Glu
65					70					75					80
Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp	Ser	Ser	Asn	Pro	Leu	Thr
				85					90					95	
Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Gly	Glu	Gly	Thr	Ser	Thr
			100					105					110		
Gly	Ser	Gly	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Ala	Asp	Asp	Val	Gln	Leu
		115					120					125			
Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala	Ser	Val	Lys	Val
	130					135					140				
Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Arg	Tyr	Thr	Met	His	Trp
145					150					155					160
Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Asn
				165					170					175	
Pro	Ser	Arg	Gly	Tyr	Thr	Asn	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe
			180					185					190		
Thr	Ile	Thr	Thr	Asp	Lys	Ser	Thr	Ser	Thr	Ala	Tyr	Met	Glu	Leu	Ser
		195					200					205			
Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Thr	Tyr	Tyr	Cys	Ala	Arg	Tyr	Tyr
	210					215					220				
Asp	Asp	His	Tyr	Cys	Leu	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr
225					230					235					240

Val Ser Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln Ser
245 250 255

Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys Lys
260 265 270

Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys Gln
275 280 285

Arg Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg Ile
290 295 300

Gly Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr
305 310 315 320

Ala Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr
325 330 335

Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr Asp
340 345 350

Thr Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val
355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Glu Leu Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val
385 390 395 400

Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu
405 410 415

Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro
420 425 430

Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
435 440 445

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
450 455 460

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys
465 470 475 480

Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu
 485 490 495

Glu Ile Lys

<210> 292
 <211> 1497
 <212> DNA
 <213> artificial sequence

<220>
 <223> VL2/VH5x4-7 LHLH

<400> 292
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 aaggcaccca aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctcgc 180
 tticagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa 240
 gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cggtggcggg 300
 accaaggtgg agatcaaagg cgaaggtact agtactgggt ctggtggaag tggaggttca 360
 ggtggagcag acgacgtcca actggtgcag tcaggggctg aagtgaaaaa acctggggcc 420
 tcagtgaagg tgcctgcaa ggcttctggc tacaccttta ctaggtacac gatgcactgg 480
 gtaaggcagg cacctggaca gggctctggaa tggattggat acattaatcc tagccgtggg 540
 tatactaatt acgcagacag cgtcaagggc cgcttcacia tcactacaga caaatccacc 600
 agcacagcct acatggaact gagcagcctg cgcttctgagg aactgcaac ctattactgt 660
 gcaagatatt atgatgatca ttactgcctt gactactggg gccaaaggcac cacggtcacc 720
 gtctcctccg gaggtgggtg atccgagctc gtgatgacct agactccact ctccctgcct 780
 gtcagtcttg gagatcaagc ctccatctct tgcagatcta gtcagagcct tgtacacagt 840
 aatggaaaca cctatttaca ttggtacctg cagaagccag gccagtctcc aaagctcctg 900
 atctacaaag tttccaaccg attttctggg gtcccagaca ggttcagtgg cagtggatca 960
 gggacagatt tcacactcaa gatcagcaga gtggaggctg aggatctggg agtttatttc 1020
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 ggtgggtggg gttctggcgg cggcggctcc ggtgggtggg gttctgaggt gcagctgctc 1140
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 tctggctaca ccttcacaaa ctatggttta agctgggtga agcagaggcc tggacaggtc 1260

cttgagtgga ttggagaggt ttatcctaga attggtaatg cttactacaa tgagaagttc 1320
aagggcaagg ccacactgac tgcagacaaa tcctccagca cagcgtccat ggagctccgc 1380
agcctgacct ctgaggactc tgcgggtctat ttctgtgcaa gacggggatc ctacgatact 1440
aactacgact ggtacttcga tgtctggggc caagggacca cggtcaccgt ctcctca 1497

<210> 293
<211> 499
<212> PRT
<213> artificial sequence

<220>
<223> VL2/VH5x4-7 LHLH

<400> 293

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
100 105 110

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
115 120 125

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
145 150 155 160

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
 165 170 175

Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe
 180 185 190

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
 195 200 205

Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr
 210 215 220

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
 225 230 235 240

Val Ser Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Thr Pro
 245 250 255

Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg
 260 265 270

Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp
 275 280 285

Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val
 290 295 300

Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser
 305 310 315 320

Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu
 325 330 335

Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly
 340 345 350

Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly
 355 360 365

Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln Ser Gly
 370 375 380

Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala
 385 390 395 400

Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys Gln Arg
405 410 415

Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg Ile Gly
420 425 430

Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala
435 440 445

Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr Ser
450 455 460

Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr Asp Thr
465 470 475 480

Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val Thr
485 490 495

Val Ser Ser

<210> 294
<211> 1497
<212> DNA
<213> artificial sequence

<220>
<223> VL3VH5x4-7 LHHL

<400> 294
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aaggcaccca aaagatggat ttatgacaca tccaaagtgg cttctggagt cctgctcgc 180
ttcagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa 240
gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cggtggcggg 300
accaaggtgg agatcaaagg cgaaggtact agtactgggt ctggtggaag tggaggttca 360
ggtggagcag acgacgtcca actggtgcag tcaggggctg aagtgaaaaa acctggggcc 420
tcagtgaagg tgtcctgcaa ggcttctggc tacaccttta ctaggtacac gatgcactgg 480
gtaaggcagg cacctggaca gggctctggaa tggattggat acattaatcc tagccgtgg 540
tatactaatt acgcagacag cgtcaagggc cgcttcacia tcactacaga caaatccacc 600

agcacagcct acatggaact gagcagcctg cgttctgagg aactgcaac ctattactgt 660
gcaagatatt atgatgatca ttactgcctt gactactggg gccaaaggcac cacggtcacc 720
gtctcctccg gaggtggtgg atccgaggtg cagctgctcg agcagtctgg agctgagctg 780
gcgaggcctg gggcttcagt gaagctgtcc tgcaaggctt ctggctacac cttcacaac 840
tatggtttaa gctgggtgaa gcagaggcct ggacaggctc ttgagtggat tggagaggtt 900
tattctagaa ttggtaatgc ttactacaat gagaagttca agggcaaggc cacactgact 960
gcagacaaat cctccagcac agcgtccatg gagctccgca gcctgacctc tgaggactct 1020
gcggtctatt tctgtgcaag acgggggatcc tacgatacta actacgactg gtacttcgat 1080
gtctggggcc aaggggaccac ggtcaccgtc tctcaggtg gtggtggttc tggcggcggc 1140
ggctccggtg gtggtggttc tgagctcgtg atgaccaga ctccactctc cctgcctgtc 1200
agtcttgag atcaagctc catctcttgc agatctagtc agagccttgt acacagtaat 1260
ggaaacacct atttacattg gtacctgcag aagccaggcc agtctccaaa gctcctgatc 1320
taciaagttt ccaaccgatt ttctggggtc ccagacaggt tcagtggcag tggatcaggg 1380
acagatttca cactcaagat cagcagagtg gaggtgagg atctgggagt ttatttctgc 1440
tctcaaagta cacatgttcc gtacacgttc ggagggggga ccaagcttga gatcaaa 1497

<210> 295

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> VL3/VH5x4-7 LHHL

<400> 295

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
100 105 110

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
115 120 125

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
145 150 155 160

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
165 170 175

Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe
180 185 190

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
195 200 205

Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr
210 215 220

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
225 230 235 240

Val Ser Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln Ser
245 250 255

Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys Lys
260 265 270

Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys Gln
275 280 285

Arg Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg Ile
290 295 300

Gly Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr

<220>
<223> VH5VL3x4-7 HLHL

<400> 296.

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cctggacagg gtctggaatg gattggatac attaatccta gccgtgggta tactaattac	180
gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac	240
atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat	300
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc	360
gaaggacta gtactgggtc tgggtggaagt ggaggttcag gtggagcaga cgacattgta	420
ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgacctgc	480
agagccagtt caagtgtaag ttacatgaac tgggtaccagc agaagccggg caaggcaccc	540
aaaagatgga tttatgacac atccaaagtg gcttctggag tccttgctcg cttcagtggc	600
agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc	660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcgggtggcgg gaccaagggtg	720
gagatcaaat ccggagggtg tggatccgag gtgcagctgc tcgagcagtc tggagctgag	780
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aactatggtt taagctgggt gaagcagagg cctggacagg tccttgagtg gattggagag	900
gtttatccta gaattggtaa tgcttactac aatgagaagt tcaagggcaa ggccacactg	960
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tctgcggtct atttctgtgc aagacgggga tcctacgata ctaactacga ctggtacttc	1080
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gtcagtcttg gagatcaagc ctccatctct tgcagatcta gtcagagcct tgtacacagt	1260
aatggaaaca cctatttaca ttggtacctg cagaagccag gccagtctcc aaagctcctg	1320
atctacaaag tttccaaccg attttctggg gtcccagaca gggttcagtgg cagtggatca	1380
gggacagatt tcacactcaa gatcagcaga gtggaggctg aggatctggg agttttatttc	1440
tgctctcaaa gtacacatgt tccgtacacg ttcggagggg ggaccaagct tgagatcaaa	1500
cat	1503

<210> 297

<211> 500

<212> PRT

<213> artificial sequence

<220>

<223> VH5VL3x4-7 HLHL

<400> 297

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys
145 150 155 160

Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln
 245 250 255

Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys
 260 265 270

Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys
 275 280 285

Gln Arg Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg
 290 295 300

Ile Gly Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu
 305 310 315 320

Thr Ala Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu
 325 330 335

Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr
 340 345 350

Asp Thr Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr
 355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 370 375 380

Gly Gly Gly Ser Glu Leu Val Met Thr Gln Thr Pro Leu Ser Leu Pro
 385 390 395 400

Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
 405 410 415

Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys
 420 425 430

Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe
 435 440 445

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe

450

455

460

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe
465 470 475 480

Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys
485 490 495

Leu Glu Ile Lys
500

<210> 298

<211> 1497

<212> DNA

<213> artificial sequence

<220>

<223> VL3VH5x4-7 LHLH

<400> 298

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aaggcaccca aaagatggat ttatgacaca tccaaagtgg cttctggagt ccttgctcgc 180
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gtctcctccg gaggtggtgg atccgagctc gtgatgacct agactccact ctccctgcct 780
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atctacaaag tttccaaccg attttctggg gtcccagaca ggttcagtgg cagtggatca 960
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tctggctaca ccttcacaaa ctatggttta agctgggtga agcagaggcc tggacaggtc 1260
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<210> 299
<211> 499
<212> PRT
<213> artificial sequence

<220>
<223> VL3/VH5x4-7 LHLH

<400> 299

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
100 105 110

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
115 120 125

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val

130

135

140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
145 150 155 160

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
165 170 175

Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe
180 185 190

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
195 200 205

Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr
210 215 220

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
225 230 235 240

Val Ser Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Thr Pro
245 250 255

Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg
260 265 270

Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp
275 280 285

Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val
290 295 300

Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser
305 310 315 320

Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu
325 330 335

Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly
340 345 350

Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly
355 360 365

Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln Ser Gly
370 375 380

Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala
385 390 395 400

Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys Gln Arg
405 410 415

Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg Ile Gly
420 425 430

Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala
435 440 445

Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr Ser
450 455 460

Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr Asp Thr
465 470 475 480

Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val Thr
485 490 495

Val Ser Ser

<210> 300
<211> 1500
<212> DNA
<213> artificial sequence

<220>
<223> VH5VL3x4-7 HLLH

<400> 300
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cctggacagg gtctggaatg gattggatac attaataccta gccgtgggtta tactaattac 180
gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 240
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gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctcctcaggc 360
gaagggtacta gtactgggtc tgggtggaagt ggagggttcag gtggagcaga cgacattgta 420

ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgacctgc 480
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acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaaggtg 720
gagatcaaatt ccggaggtgg tggatccgag ctctgtgatga cccagactcc actctccctg 780
cctgtcagtc ttggagatca agcctccatc tcttgagat ctatgcagag ccttgtagac 840
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cgcagcctga cctctgagga ctctgcggtc tatttctgtg caagacgggg atcctacgat 1440
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<210> 301
<211> 500
<212> PRT
<213> artificial sequence

<220>
<223> VH5VL3x4-7 HLLH

<400> 301

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
 85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
 115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
 130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys
 145 150 155 160

Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Thr
 245 250 255

Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys
 260 265 270

Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His
 275 280 285

Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys
290 295 300

Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
305 310 315 320

Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp
325 330 335

Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe
340 345 350

Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly
355 360 365

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln Ser
370 375 380

Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys Lys
385 390 395 400

Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys Gln
405 410 415

Arg Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg Ile
420 425 430

Gly Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr
435 440 445

Ala Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr
450 455 460

Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr Asp
465 470 475 480

Thr Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val
485 490 495

Thr Val Ser Ser
500

<210> 302
<211> 1497

<212> DNA

<213> artificial sequence

<220>

<223> VL1VH7x4-7 LHHL

<400> 302

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aaggcaccga aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctcgc	180
ttcagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa	240
gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cgggtggcggg	300
accaaggtgg agatcaaagg cgaaggtact agtactgggt ctggtggaag tggaggttca	360
ggtggagcag acgacgtcca actggtgcag tcaggggctg aagtgaaaaa acctggggcc	420
tcagtgaagg tgtcctgcaa ggcttctggc tacaccttta ctaggtacac gatgcactgg	480
gtaaggcagg cacctggaca gggctctggaa tggattggat acattaatcc tagccgtggg	540
tatactaatt acaatcagaa gttcaaggac cgcgtcacia tcactacaga caaatccacc	600
agcacagcct acatggaact gagcagcctg cgttctgagg aactgcagt ctattactgt	660
gcaagatatt atgatgatca ttactgcctt gactactggg gccaaaggcac cacggtcacc	720
gtctcctccg gaggtgggtg atccgaggtg cagctgctcg agcagtctgg agctgagctg	780
gcgaggcctg gggcttcagt gaagctgtcc tgcaaggctt ctggctacac cttcaciaaac	840
tatgggttta gctgggtgaa gcagaggcct ggacaggtcc ttgagtggat tggagaggtt	900
tatcctagaa ttggtaatgc ttactacaat gagaagttca agggcaaggc cacactgact	960
gcagacaaat cctccagcac agcgtccatg gagctccgca gcctgacctc tgaggactct	1020
gcgggtctatt tctgtgcaag acgggggatcc tacgatacta actacgactg gtacttcgat	1080
gtctggggcc aagggaccac ggtcacctgc tcctcaggtg gtgggtgggtc tggcggcggc	1140
ggctccggtg gtgggtgggtc tgagctcgtg atgaccaga ctccactctc cctgcctgtc	1200
agtcttggag atcaagcctc catctcttgc agatctagtc agagccttgt acacagtaat	1260
ggaaacacct atttacattg gtacctgcag aagccaggcc agtctccaaa gctcctgatc	1320
tacaaagttt ccaaccgatt ttctggggtc ccagacaggt tcagtggcag tggatcaggg	1380
acagatttca cactcaagat cagcagagtg gaggtgagg atctgggagt ttatttctgc	1440
tctcaaagta cacatgttcc gtacacgttc ggagggggga ccaagcttga gatcaaa	1497

<210> 303

<211> 499
<212> PRT
<213> artificial sequence

<220>
<223> VL1VH7x4-7 LHHL

<400> 303

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
100 105 110

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
115 120 125

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
145 150 155 160

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
165 170 175

Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
180 185 190

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
195 200 205

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr
210 215 220

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
225 230 235 240

Val Ser Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln Ser
245 250 255

Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys Lys
260 265 270

Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys Gln
275 280 285

Arg Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg Ile
290 295 300

Gly Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr
305 310 315 320

Ala Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr
325 330 335

Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr Asp
340 345 350

Thr Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val
355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Glu Leu Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val
385 390 395 400

Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu
405 410 415

Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro
420 425 430

Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser

435

440

445

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
450 455 460

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys
465 470 475 480

Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu
485 490 495

Glu Ile Lys

<210> 304
<211> 1500
<212> DNA
<213> artificial sequence

<220>
<223> VH7-VL1x4-7 HLHL

<400> 304
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cctggacagg gtctggaatg gattggatac attaataccta gccgtgggtta tactaattac 180
aatcagaagt tcaaggaccg cgtcaccaatc actacagaca aatccaccag cacagcctac 240
atggaactga gcagcctgcg ttctgaggac actgcagtct attactgtgc aagatattat 300
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctcctcaggc 360
gaaggtaacta gtactgggttc tgggtggaagt ggagggttcag gtggagcaga cgacattcag 420
atgacccagt ctccatctag cctgtctgca tctgtcgggg accgtgtcac catcacctgc 480
agagccagtc aaagtgtaag ttacatgaac tgggtaccagc agaagccggg caaggcaccc 540
aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaaggtg 720
gagatcaaatt ccggaggtgg tggatccgag gtgcagctgc tcgagcagtc tggagctgag 780
ctggcgaggc ctggggcttc agtgaagctg tcctgcaagg cttctggcta caccttcaca 840
aactatggtt taagctgggt gaagcagagg cctggacagg tccttgagtg gattggagag 900
gtttatccta gaattggtaa tgcttactac aatgagaagt tcaagggcaa ggccacactg 960

actgcagaca aatcctccag cacagcgtcc atggagctcc gcagcctgac ctctgaggac 1020
tctgcggtct atttctgtgc aagacgggga tcctacgata ctaactacga ctggtacttc 1080
gatgtctggg gccaaaggac cacggtcacc gtctcctcag gtggtggtgg ttctggcggc 1140
ggcggtccg gtggtggtgg ttctgagctc gtgatgacc agactccact ctccctgcct 1200
gtcagtcttg gagatcaagc ctccatctct tgcagatcta gtcagagcct tgtacacagt 1260
aatggaaaca cctattttaca ttggtacctg cagaagccag gccagtctcc aaagctcctg 1320
atctacaaag tttccaaccg attttctggg gtcccagaca ggttcagtgg cagtggatca 1380
gggacagatt tcacactcaa gatcagcaga gtggaggctg aggatctggg agtttatttc 1440
tgctctcaaa gtacacatgt tccgtacacg ttccggagggg ggaccaagct tgagatcaaa 1500

<210> 305
<211> 500
<212> PRT
<213> artificial sequence

<220>
<223> VH7-VL1x4-7 HLHL

<400> 305

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly

115

120

125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser
 130 135 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
 145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln
 245 250 255

Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys
 260 265 270

Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys
 275 280 285

Gln Arg Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg
 290 295 300

Ile Gly Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu
 305 310 315 320

Thr Ala Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu
 325 330 335

Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr
 340 345 350

Asp Thr Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr
 355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 370 375 380

Gly Gly Gly Ser Glu Leu Val Met Thr Gln Thr Pro Leu Ser Leu Pro
 385 390 395 400

Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
 405 410 415

Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys
 420 425 430

Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe
 435 440 445

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
 450 455 460

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe
 465 470 475 480

Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys
 485 490 495

Leu Glu Ile Lys
 500

<210> 306
 <211> 1497
 <212> DNA
 <213> artificial sequence

<220>
 <223> VL1-VH7x4-7 LHLH

<400> 306
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 atcacctgca gagccagtca aagtgttaagt tacatgaact ggtaccagca gaagccgggc 120
 aaggcaccga aaagatggat ttatgacaca tccaaagtgg cttctggagt ccttgctcgc 180
 ttcagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa 240
 gatgctgcc cttattactg ccaacagtgg agtagtaacc cgctcacgtt cgggtggcggg 300

accaaggtgg agatcaaagg cgaaggtact agtactgggt ctggtggaag tggaggttca 360
ggtggagcag acgacgtcca actggtgcag tcaggggctg aagtgaaaaa acctggggcc 420
tcagtgaagg tgtcctgcaa ggcttctggc tacaccttta ctaggtacac gatgcactgg 480
gtaaggcagg cacctggaca gggctctggaa tggattggat acattaatcc tagccgtggt 540
tatactaatt acaatcagaa gttcaaggac cgcgtcacia tcactacaga caaatccacc 600
agcacagcct acatggaact gagcagcctg cgttctgagg aactgcagt ctattactgt 660
gcaagatatt atgatgatca ttactgcctt gactactggg gccaaaggcac cacggtcacc 720
gtctcctccg gaggtggtgg atccgagctc gtgatgacct agactccact ctccctgcct 780
gtcagtcttg gagatcaagc ctccatctct tgcagatcta gtcagagcct tgtacacagt 840
aatggaaaca cctatttaca ttggtacctg cagaagccag gccagtctcc aaagctectg 900
atctacaaag tttccaaccg attttctggg gtcccagaca ggttcagtgg cagtggatca 960
gggacagatt tcacactcaa gatcagcaga gtggaggctg aggatctggg agtttatttc 1020
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ggtggtggtg gttctggcgg cggcggctcc ggtggtggtg gttctgaggt gcagctgctc 1140
gagcagtctg gagctgagct ggcgaggcct ggggcttcag tgaagctgtc ctgcaaggct 1200
tctggctaca ccttcacaaa ctatggttta agctgggtga agcagaggcc tggacaggtc 1260
cttgagtgga ttggagaggt ttatcctaga attggtaatg ctactacaa tgagaagttc 1320
aagggaagg ccacactgac tgcagacaaa tcctccagca cagcgtccat ggagctccgc 1380
agcctgacct ctgaggactc tgcggtctat ttctgtgcaa gacggggatc ctacgatact 1440
aactacgact ggtacttcga tgtctggggc caagggacca cggtcaccgt ctctca 1497

<210> 307

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> VL1-VH7x4-7 LHLH

<400> 307

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
 35 40 45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
 85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
 100 105 110

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
 115 120 125

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
 130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
 145 150 155 160

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
 165 170 175

Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
 180 185 190

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
 195 200 205

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr
 210 215 220

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
 225 230 235 240

Val Ser Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Thr Pro
 245 250 255

Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg
 260 265 270

Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp
275 280 285

Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val
290 295 300

Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser
305 310 315 320

Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu
325 330 335

Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly
340 345 350

Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly
355 360 365

Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln Ser Gly
370 375 380

Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala
385 390 395 400

Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys Gln Arg
405 410 415

Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg Ile Gly
420 425 430

Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala
435 440 445

Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr Ser
450 455 460

Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr Asp Thr
465 470 475 480

Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val Thr
485 490 495

Val Ser Ser

<210> 308
<211> 1500
<212> DNA
<213> artificial sequence

<220>
<223> VH7-VL1x4-7 HLLH

<400> 308
gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaagggtg 60
tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 120
cctggacagg gtctggaatg gattggatac attaatccta gccgtgggtta tactaattac 180
aatcagaagt tcaaggaccg cgtcacaatc actacagaca aatccaccag cacagcctac 240
atggaactga gcagcctgcg ttctgaggac actgcagtct attactgtgc aagatattat 300
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc 360
gaagggtacta gtactgggtc tgggtggaagt ggagggttcag gtggagcaga cgacattcag 420
atgaccagct ctccatctag cctgtctgca tctgtcgggg accgtgtcac catcacctgc 480
agagccagtc aaagtgtaag ttacatgaac tggtagcagc agaagccggg caaggcaccc 540
aaaagatgga tttatgacac atccaaagtg gcttctggag tcctgtctcg cttcagtggc 600
agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcgggtggcgg gaccaagggtg 720
gagatcaaata ccggagggtg tggatccgag ctctgtgatga ccagactcc actctccctg 780
cctgtcagtc ttggagatca agcctccatc tcttgagat ctatgcagag ccttgtagac 840
agtaatggaa acacctatctt acattggtac ctgcagaagc caggccagtc tccaaagctc 900
ctgatctaca aagtttccaa ccgattttct ggggtcccag acagggttcag tggcagtggg 960
tcaggggacag atttcacact caagatcagc agagtggagg ctgaggatct gggagtttat 1020
ttctgtcttc aaagtacaca tgttccgtac acgttcggag gggggaccaa gcttgagatc 1080
aaagggtggtg gtggttctgg cggcggcggc tccggtggtg gtggttctga ggtgcagctg 1140
ctcgagcagt ctggagctga gctggcgagg cctggggctt cagtgaagct gtcctgcaag 1200
gcttctgggt acaccttcac aaactatggt ttaagctggg tgaagcagag gcctggacag 1260
gtccttgagt ggattggaga ggtttatcct agaattggta atgcttacta caatgagaag 1320
ttcaagggca aggccacact gactgcagac aaatcctcca gcacagcgtc catggagctc 1380
cgcagcctga cctctgagga ctctgcggtc tatttctgtg caagacgggg atcctacgat 1440

actaactacg actggtactt cgatgtctgg ggccaagggg ccacgggtcac cgtctcctca 1500

<210> 309

<211> 500

<212> PRT

<213> artificial sequence

<220>

<223> VH7-VL1x4-7 HLLH

<400> 309

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser
130 135 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Thr
245 250 255

Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys
260 265 270

Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His
275 280 285

Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys
290 295 300

Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
305 310 315 320

Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp
325 330 335

Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe
340 345 350

Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly
355 360 365

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln Ser
370 375 380

Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys Lys
385 390 395 400

Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys Gln
405 410 415

Arg Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg Ile

420

425

430

Gly Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr
435 440 445

Ala Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr
450 455 460

Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr Asp
465 470 475 480

Thr Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val
485 490 495

Thr Val Ser Ser
500

<210> 310

<211> 1497

<212> DNA

<213> artificial sequence

<220>

<223> VL2VH7x4-7 LHHL

<400> 310

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aaggcaccga aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctcgc 180
ttcagtggca gtgggtctgg gaccgactac tctctcaca tcaacagctt ggaggctgaa 240
gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cgggtggcggg 300
accaaggtgg agatcaaagg cgaaggtact agtactgggt ctggtggaag tggaggttca 360
gggtggagcag acgacgtcca actggtgcag tcaggggctg aagtgaaaaa acctgggggc 420
tcagtgaagg tgtcctgcaa ggcttctggc tacaccttta ctaggtacac gatgcactgg 480
gtaaggcagg cacctggaca gggctctggaa tggattggat acattaatcc tagccgtggg 540
tatactaatt acaatcagaa gttcaaggac cgcgtcaca tcactacaga caaatccacc 600
agcacagcct acatggaact gagcagcctg cggttctgagg aactgcagt ctattactgt 660
gcaagatatt atgatgatca ttactgcctt gactactggg gccaaaggcac cacggtcacc 720
gtctcctccg gaggtgggtg atccgaggtg cagctgctcg agcagtctgg agctgagctg 780
gcgaggcctg gggcttcagt gaagctgtcc tgcaaggctt ctggctacac cttcacaac 840

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tattcctagaa ttggtaatgc ttactacaat gagaagttca agggcaaggc cacactgact 960
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agtcttggag atcaagcctc catctcttgc agatctagtc agagccttgt acacagtaat 1260
ggaaacacct atttacattg gtacctgcag aagccaggcc agtctccaaa gctcctgatc 1320
taciaaagttt ccaaccgatt ttctggggtc ccagacaggt tcagtggcag tggatcaggg 1380
acagatttca cactcaagat cagcagagtg gaggctgagg atctgggagt ttatttctgc 1440
tctcaaagta cacatgttcc gtacacgttc ggagggggga ccaagcttga gatcaaa 1497

<210> 311
<211> 499
<212> PRT
<213> artificial sequence

<220>
<223> VL2VH7x4-7 LHHL

<400> 311

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr

100	105	110
Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu 115 120 125		
Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val 130 135 140		
Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp 145 150 155 160		
Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn 165 170 175		
Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val 180 185 190		
Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser 195 200 205		
Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr 210 215 220		
Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr 225 230 235 240		
Val Ser Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln Ser 245 250 255		
Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys Lys 260 265 270		
Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys Gln 275 280 285		
Arg Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg Ile 290 295 300		
Gly Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr 305 310 315 320		
Ala Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr 325 330 335		

Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr Asp
 340 345 350

Thr Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val
 355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 370 375 380

Gly Gly Ser Glu Leu Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val
 385 390 395 400

Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu
 405 410 415

Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro
 420 425 430

Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
 435 440 445

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 450 455 460

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys
 465 470 475 480

Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu
 485 490 495

Glu Ile Lys

<210> 312
 <211> 1500
 <212> DNA
 <213> artificial sequence

<220>
 <223> VH7VL2x4-7 HLHL

<400> 312
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 cctggacagg gtctggaatg gattggatac attaatccta gccgtgggta tactaattac 180

aatcagaagt tcaaggaccg cgtcacaaatc actacagaca aatccaccag cacagcctac 240
atggaactga gcagcctgcg ttctgaggac actgcagtct attactgtgc aagatattat 300
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctcctcaggc 360
gaaggtacta gtactgggtc tgggtggaagt ggaggttcag gtggagcaga cgacattgta 420
ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc 480
agagccagtc aaagtgtgaa ttacatgaac tgggtaccagc agaagccggg caaggcaccc 540
aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaaggtg 720
gagatcaaat ccggagggtg tggatccgag gtgcagctgc tcgagcagtc tggagctgag 780
ctggcgaggc ctggggcttc agtgaagctg tcctgcaagg cttctggcta caccttcaca 840
aactatggtt taagctgggt gaagcagagg cctggacagg tccttgagtg gattggagag 900
gtttatccta gaattggtaa tgcttactac aatgagaagt tcaagggcaa ggccacactg 960
actgcagaca aatcctccag cacagcgtcc atggagctcc gcagcctgac ctctgaggac 1020
tctgcggtct atttctgtgc aagacgggga tcctacgata ctaactacga ctggtacttc 1080
gatgtctggg gccaaaggac cacggtcacc gtctcctcag gtggtggtgg ttctggcggc 1140
ggcggctccg gtggtggtgg ttctgagctc gtgatgacc agactccact ctccctgcct 1200
gtcagtcttg gagatcaagc ctccatctct tgcagatcta gtcagagcct tgtacacagt 1260
aatggaaaca cctattttaca ttggtacctg cagaagccag gccagtctcc aaagctcctg 1320
atctacaaag tttccaaccg attttctggg gtcccagaca ggttcagtgg cagtggatca 1380
gggacagatt tcacactcaa gatcagcaga gtggaggctg aggatctggg agtttatttc 1440
tgctctcaaa gtacacatgt tccgtacacg ttcggagggg ggaccaagct tgagatcaaa 1500

<210> 313
<211> 500
<212> PRT
<213> artificial sequence

<220>
<223> VH7VL2x4-7 HLHL

<400> 313

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln
245 250 255

Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys
260 265 270

Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys
275 280 285

Gln Arg Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg
290 295 300

Ile Gly Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu
305 310 315 320

Thr Ala Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu
325 330 335

Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr
340 345 350

Asp Thr Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr
355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
370 375 380

Gly Gly Gly Ser Glu Leu Val Met Thr Gln Thr Pro Leu Ser Leu Pro
385 390 395 400

Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
405 410 415

Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys
420 425 430

Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe
435 440 445

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
450 455 460

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe
465 470 475 480

Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys
485 490 495

Leu Glu Ile Lys
500

<210> 314
<211> 1497
<212> DNA
<213> artificial sequence

<220>
<223> VL2VH7x4-7 LHLH

<400> 314
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aaggcaccca aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctcgc 180
ttcagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa 240
gatgctgcc cttattactg ccaacagtgg agtagtaacc cgctcacgtt cggtggcggg 300
accaaggtgg agatcaaagg cgaaggtact agtactgggt ctggtggaag tggagggttca 360
ggtggagcag acgacgtcca actggtgcag tcaggggctg aagtgaaaaa acctggggcc 420
tcagtgaagg tgcctgcaa ggcttctggc tacaccttta ctaggtacac gatgcactgg 480
gtaaggcagg cacctggaca gggctctggaa tggattggat acattaatcc tagccgtggg 540
tatactaatt acaatcagaa gttcaaggac cgcgtcacia tcactacaga caaatccacc 600
agcacagcct acatggaact gagcagcctg cgcttctgagg aactgcagt ctattactgt 660
gcaagatatt atgatgatca ttactgcctt gactactggg gccaaggcac cacggtcacc 720
gtctcctccg gaggtgggtg atccgagctc gtgatgacct agactccact ctccctgcct 780
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aagggcaagg ccacactgac tgcagacaaa tcctccagca cagcggtccat ggagctccgc 1380

agcctgacct ctgaggactc tgcggtctat ttctgtgcaa gacggggatc ctacgatact 1440

aactacgact ggtacttcga tgtctggggc caagggacca cggtcacccgt ctctca 1497

<210> 315

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> VL2VH7x4-7 LHLH

<400> 315

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
100 105 110

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
115 120 125

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
145 150 155 160

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
165 170 175

Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
180 185 190

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
195 200 205

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr
210 215 220

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
225 230 235 240

Val Ser Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Thr Pro
245 250 255

Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg
260 265 270

Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp
275 280 285

Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val
290 295 300

Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser
305 310 315 320

Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu
325 330 335

Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly
340 345 350

Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly
355 360 365

Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln Ser Gly
370 375 380

Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala
385 390 395 400

Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys Gln Arg

405

410

415

Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg Ile Gly
420 425 430

Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala
435 440 445

Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr Ser
450 455 460

Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr Asp Thr
465 470 475 480

Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val Thr
485 490 495

Val Ser Ser

<210> 316
<211> 1500
<212> DNA
<213> artificial sequence

<220>
<223> VH7VL2x4-7 HLLH

<400> 316
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cctggacagg gtctggaatg gattggatac attaataccta gccgtgggtta tactaattac 180
aatcagaagt tcaaggaccg cgtcacaatc actacagaca aatccaccag cacagcctac 240
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gaaggctacta gtactgggtc tgggtggaagt ggagggttcag gtggagcaga cgacattgta 420
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aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaagggtg 720

gagatcaaat ccggaggtgg tggatccgag ctctgtgatga cccagactcc actctccctg 780
 cctgtcagtc ttggagatca agcctccatc tcttgcagat ctatgcagag ccttgtacac 840
 agtaatggaa acacctatatt acattggtac ctgcagaagc caggccagtc tccaaagctc 900
 ctgatctaca aagtttccaa ccgattttct ggggtcccag acaggttcag tggcagtgga 960
 tcagggacag atttcacact caagatcagc agagtggagg ctgaggatct gggagtattat 1020
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 gcttctggct acaccttcac aaactatggt ttaagctggg tgaagcagag gcctggacag 1260
 gtccttgagt ggattggaga ggtttatcct agaattggta atgcttacta caatgagaag 1320
 ttcaagggca aggccacact gactgcagac aaatcctcca gcacagcgtc catggagctc 1380
 cgcagcctga cctctgagga ctctgcggtc tatttctgtg caagacgggg atcctacgat 1440
 actaactacg actggtactt cgatgtctgg ggccaaggga ccacggtcac cgtctcctca 1500

<210> 317

<211> 500

<212> PRT

<213> artificial sequence

<220>

<223> VH7VL2x4-7 HLLH

<400> 317

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
 50 55 60

Lys Asp Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
 115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
 130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
 145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Thr
 245 250 255

Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys
 260 265 270

Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His
 275 280 285

Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys
 290 295 300

Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
 305 310 315 320

Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp
 325 330 335

Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe
 340 345 350

Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly
 355 360 365

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln Ser
 370 375 380

Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys Lys
 385 390 395 400

Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys Gln
 405 410 415

Arg Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg Ile
 420 425 430

Gly Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr
 435 440 445

Ala Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr
 450 455 460

Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr Asp
 465 470 475 480

Thr Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val
 485 490 495

Thr Val Ser Ser
 500

<210> 318
 <211> 1497
 <212> DNA
 <213> artificial sequence

<220>
 <223> VL3VH7x4-7 LHHL

<400> 318
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ctgacctgca gagccagttc aagtgttaagt tacatgaact ggtaccagca gaagccgggc 120
aaggcacca aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctcgc 180
ttcagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa 240
gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cgggtggcggg 300
accaaggtgg agatcaaagg cgaaggtact agtactgggt ctggtggaag tggaggttca 360
ggtggagcag acgacgtcca actggtgcag tcaggggctg aagtgaaaaa acctggggcc 420
tcagtgaagg tgtcctgcaa ggcttctggc tacaccttta ctaggtacac gatgcactgg 480
gtaaggcagg cacctggaca gggctctggaa tggattggat acattaatcc tagccgtggg 540
tatactaatt acaatcagaa gttcaaggac cgcgtcacia tcactacaga caaatccacc 600
agcacagcct acatggaact gagcagcctg cgctctgagg aactgcagt ctattactgt 660
gcaagatatt atgatgatca ttactgcctt gactactggg gccaaaggcac cacggtcacc 720
gtctcctccg gaggtgggtg atccgaggtg cagctgctcg agcagtctgg agctgagctg 780
gcgaggcctg gggcttcagt gaagctgtcc tgcaaggctt ctggctacac cttcaciaaac 840
tatggtttaa gctgggtgaa gcagaggcct ggacagggtc ttgagtggat tggagagggt 900
tatcctagaa ttggtaatgc ttactacaat gagaagttca agggcaaggc cacactgact 960
gcagacaaat cctccagcac agcgtccatg gagctccgca gcctgacctc tgaggactct 1020
gcgggtctatt tctgtgcaag acgggggatcc tacgatacta actacgactg gtacttcgat 1080
gtctggggcc aagggaccac ggtcaccgtc tcctcagggt gtggtgggtc tggcggcggc 1140
ggctccgggt gtggtgggtc tgagctcgtg atgaccaga ctccactctc cctgcctgtc 1200
agtcttggag atcaagcctc catctcttgc agatctagtc agagccttgt acacagtaat 1260
ggaaacacct atttacattg gtacctgcag aagccaggcc agtctccaaa gctcctgatc 1320
taciaaagttt ccaaccgatt ttctgggggtc ccagacaggt tcagtggcag tggatcaggg 1380
acagatttca cactcaagat cagcagagtg gaggtgagg atctgggagt ttatttctgc 1440
tctcaaagta cacatgttcc gtacacgttc ggagggggga ccaagcttga gatcaaa 1497

<210> 319

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> VL3VH7x4-7 LHHL

<400> 319

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
100 105 110

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
115 120 125

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
145 150 155 160

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
165 170 175

Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
180 185 190

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
195 200 205

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr
210 215 220

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
225 230 235 240

Val Ser Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln Ser
245 250 255

Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys Lys
260 265 270

Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys Gln
275 280 285

Arg Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg Ile
290 295 300

Gly Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr
305 310 315 320

Ala Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr
325 330 335

Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr Asp
340 345 350

Thr Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val
355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Glu Leu Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val
385 390 395 400

Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu
405 410 415

Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro
420 425 430

Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
435 440 445

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
450 455 460

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys
465 470 475 480

Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu
485 490 495

Glu Ile Lys

<210> 320
<211> 1500
<212> DNA
<213> artificial sequence

<220>
<223> VH7VL3x4-7 HLHL

<400> 320
gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaagggtg 60
tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 120
cctggacagg gtctggaatg gattggatac attaataccta gccgtgggtta tactaattac 180
aatcagaagt tcaaggaccg cgtcacaatc actacagaca aatccaccag cacagcctac 240
atggaactga gcagcctgcg ttctgaggac actgcagtct attactgtgc aagatattat 300
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctcctcaggc 360
gaagggtacta gtactgggttc tgggtggaagt ggagggttcag gtggagcaga cgacattgta 420
ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgacctgc 480
agagccagtt caagtgtgtaag ttacatgaac tgggtaccagc agaagccggg caaggcaccc 540
aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcgggtggcgg gaccaagggtg 720
gagatcaaata ccggagggtg tggatccgag gtgcagctgc tcgagcagtc tggagctgag 780
ctggcgaggc ctggggcttc agtgaagctg tcctgcaagg cttctggcta caccttcaca 840
aactatgggt taagctgggt gaagcagagg cctggacagg tccttgagtg gattggagag 900
gtttatccta gaattggtaa tgcttactac aatgagaagt tcaagggcaa ggccacactg 960
actgcagaca aatcctccag cacagcgtcc atggagctcc gcagcctgac ctctgaggac 1020
tctgcggtct atttctgtgc aagacgggga tcctacgata ctaactacga ctggtacttc 1080
gatgtctggg gccaaaggac cacggtcacc gtctcctcag gtgggtgggtg ttctggcggc 1140
ggcggctccg gtgggtgggtg ttctgagctc gtgatgacct agactccact ctcctgcct 1200

gtcagtcttg gagatcaagc ctccatctct tgcagatcta gtcagagcct tgtacacagt 1260
aatggaaaca cctatttaca ttggtacctg cagaagccag gccagtctcc aaagctcctg 1320
atctacaaag tttccaaccg attttctggg gtcccagaca ggttcagtgg cagtggatca 1380
gggacagatt tcacactcaa gatcagcaga gtggaggctg aggatctggg agtttatttc 1440
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<210> 321
<211> 500
<212> PRT
<213> artificial sequence

<220>
<223> VH7VL3x4-7 HLHL

<400> 321

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys
145 150 155 160

Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln
245 250 255

Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys
260 265 270

Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys
275 280 285

Gln Arg Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg
290 295 300

Ile Gly Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu
305 310 315 320

Thr Ala Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu
325 330 335

Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr
340 345 350

Asp Thr Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr
355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
370 375 380

Gly Gly Gly Ser Glu Leu Val Met Thr Gln Thr Pro Leu Ser Leu Pro

385 390 395 400

Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
405 410 415

Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys
420 425 430

Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe
435 440 445

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
450 455 460

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe
465 470 475 480

Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys
485 490 495

Leu Glu Ile Lys
500

<210> 322
<211> 1497
<212> DNA
<213> artificial sequence

<220>
<223> VL3VH7x4-7 LHLH

<400> 322
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aaggcaccga aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctcgc 180
ttcagtggca gtgggtctgg gaccgactac tctctcaca tcaacagctt ggaggctgaa 240
gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cggtggcggg 300
accaaggtgg agatcaaagg cgaaggtact agtactgggt ctggtggaag tggaggttca 360
gggtggagcag acgacgtcca actggtgcag tcaggggctg aagtgaaaaa acctggggcc 420
tcagtgaagg tgtcctgcaa ggcttctggc tacaccttta ctaggtacac gatgcactgg 480
gtaaggcagg cacctggaca gggctctggaa tggattggat acattaatcc tagccgtggg 540
tatactaatt acaatcagaa gttcaaggac cgcgtcaca tcaactacaga caaatccacc 600

agcacagcct acatggaact gagcagcctg cgttctgagg aactgcagt ctattactgt 660
gcaagatatt atgatgatca ttactgcctt gactactggg gccaaaggcac cacggtcacc 720
gtctcctccg gaggtggtgg atccgagctc gtgatgacct agactccact ctccctgcct 780
gtcagtcctt gagatcaagc ctccatctct tgcagatcta gtcagagcct tgtacacagt 840
aatggaaaca cctattttaca ttggtacctg cagaagccag gccagtctcc aaagctcctg 900
atctacaaag tttccaaccg attttctggg gtcccagaca gggtcagtgg cagtggatca 960
gggacagatt tcacactcaa gatcagcaga gtggaggctg aggatctggg agtttatctt 1020
tgctctcaaa gtacacatgt tccgtacacg ttcggagggg ggaccaagct tgagatcaaa 1080
ggtggtggtg gttctggcgg cggcggctcc ggtggtggtg gttctgaggt gcagctgctc 1140
gagcagtcct gagctgagct ggcgaggcct ggggcttcag tgaagctgtc ctgcaaggct 1200
tctggctaca ccttcacaaa ctatgggtta agctgggtga agcagaggcc tggacaggctc 1260
cttgagtgga ttggagaggt ttatcctaga attggtaatg ctactacaa tgagaagttc 1320
aagggaagg ccacactgac tgcagacaaa tctccagca cagcgtccat ggagctccgc 1380
agcctgacct ctgaggactc tgcggtctat ttctgtgcaa gacggggatc ctacgatact 1440
aactacgact ggtacttcga tgtctggggc caagggacca cggtcaccgt ctctca 1497

<210> 323

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> VL3VH7x4-7 LHLH

<400> 323

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu

65		70		75		80									
Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp	Ser	Ser	Asn	Pro	Leu	Thr
			85						90					95	
Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Gly	Glu	Gly	Thr	Ser	Thr
			100					105					110		
Gly	Ser	Gly	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Ala	Asp	Asp	Val	Gln	Leu
		115					120					125			
Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala	Ser	Val	Lys	Val
	130					135					140				
Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Arg	Tyr	Thr	Met	His	Trp
145					150					155					160
Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Asn
				165					170					175	
Pro	Ser	Arg	Gly	Tyr	Thr	Asn	Tyr	Asn	Gln	Lys	Phe	Lys	Asp	Arg	Val
			180					185					190		
Thr	Ile	Thr	Thr	Asp	Lys	Ser	Thr	Ser	Thr	Ala	Tyr	Met	Glu	Leu	Ser
	195						200					205			
Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Tyr	Tyr
	210					215					220				
Asp	Asp	His	Tyr	Cys	Leu	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr
225					230					235					240
Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Glu	Leu	Val	Met	Thr	Gln	Thr	Pro
			245						250					255	
Leu	Ser	Leu	Pro	Val	Ser	Leu	Gly	Asp	Gln	Ala	Ser	Ile	Ser	Cys	Arg
			260					265					270		
Ser	Ser	Gln	Ser	Leu	Val	His	Ser	Asn	Gly	Asn	Thr	Tyr	Leu	His	Trp
		275					280					285			
Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Lys	Val
	290					295					300				

Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser
305 310 315 320

Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu
325 330 335

Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly
340 345 350

Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly
355 360 365

Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln Ser Gly
370 375 380

Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala
385 390 395 400

Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys Gln Arg
405 410 415

Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg Ile Gly
420 425 430

Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala
435 440 445

Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr Ser
450 455 460

Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr Asp Thr
465 470 475 480

Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val Thr
485 490 495

Val Ser Ser

<210> 324
<211> 1500
<212> DNA
<213> artificial sequence

<220>
<223> VH7VL3x4-7 HLLH

<400> 324

gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaagggtg	60
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cctggacagg gtctggaatg gattggatac attaataccta gccgtgggtta tactaattac	180
aatcagaagt tcaaggaccg cgtcacaatc actacagaca aatccaccag cacagcctac	240
atggaactga gcagcctgcg ttctgaggac actgcagtct attactgtgc aagatattat	300
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctcctcaggc	360
gaagg tacta gtactgggttc tgggtggaagt ggaggttcag gtggagcaga cgacattgta	420
ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgacctgc	480
agagccagtt caagtgtaag ttacatgaac tgggtaccagc agaagccggg caaggcaccc	540
aaaagatgga tttatgacac atccaaagtg gcttctggag tccttgctcg cttcagtggc	600
agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc	660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcgggtggcgg gaccaagggtg	720
gagatcaa at ccggagggtg tggatccgag ctctgtgatga ccagactcc actctccctg	780
cctgtcagtc ttggagatca agcctccatc tcttgagat ctagtacag ccttgtagac	840
agtaatggaa acacctat t acattgggtac ctgcagaagc caggccagtc tccaaagctc	900
ctgatctaca aagtttccaa ccgattttct ggggtcccag acagggttcag tggcagtggg	960
tcaggggacag atttcacact caagatcagc agagtggagg ctgaggatct gggagt t tat	1020
ttctgctctc aaagtacaca t gttccgtac acgttcggag gggggaccaa gcttgagatc	1080
aaagggtggtg gtggttctgg cggcggcggc tccggtggtg gtggttctga ggtgcagctg	1140
ctcgagcagt ctggagctga gctggcgagg cctggggcct cagtgaagct gtcctgcaag	1200
gcttctgggt acaccttcac aaactatggt ttaagctggg tgaagcagag gcctggacag	1260
gtccttgagt ggattggaga ggtttatcct agaattggta atgcttacta caatgagaag	1320
ttcaagggca aggccacact gactgcagac aaatcctcca gcacagcgtc catggagctc	1380
cgcagcctga cctctgagga ctctgcggtc tatttctgtg caagacgggg atcctacgat	1440
actaactacg actggtactt cgatgtctgg ggccaaggga ccacggtcac cgtctcctca	1500

<210> 325

<211> 500

<212> PRT

<213> artificial sequence

<220>

<223> VH7VL3x4-7 HLLH

<400> 325

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
 50 55 60

Lys Asp Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
 115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
 130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys
 145 150 155 160

Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Thr
245 250 255

Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys
260 265 270

Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His
275 280 285

Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys
290 295 300

Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
305 310 315 320

Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp
325 330 335

Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe
340 345 350

Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly
355 360 365

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln Ser
370 375 380

Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys Lys
385 390 395 400

Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys Gln
405 410 415

Arg Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg Ile
420 425 430

Gly Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr
435 440 445

Ala Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr
450 455 460

Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr Asp
465 470 475 480

Thr Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val
485 490 495

Thr Val Ser Ser
500

<210> 326
<211> 1494
<212> DNA
<213> artificial sequence

<220>
<223> VL1VH5xCD19 LHHL

<400> 326
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atcacctgca gagccagtca aagtgttaagt tacatgaact ggtaccagca gaagccgggc 120
aaggcaccga aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctcgc 180
ttcagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa 240
gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cgggtggcggg 300
accaaggtgg agatcaaagg cgaaggtact agtactgggt ctggtggaag tggagggttca 360
ggtggagcag acgacgtcca actggtgcag tcaggggctg aagtgaaaaa acctggggcc 420
tcagtgaagg tgtcctgcaa ggcttctggc tacaccttta ctaggtacac gatgcactgg 480
gtaaggcagg cacctggaca gggctctggaa tggattggat acattaatcc tagccgtggg 540
tatactaatt acgcagacag cgtcaagggc cgcttcacia tctactacaga caaatccacc 600
agcacagcct acatggaact gagcagcctg cgcttctgagg aactgcaac ctattactgt 660
gcaagatatt atgatgatca ttactgcctt gactactggg gccaaaggcac cacggtcacc 720
gtctcctccg gaggtgggtg atcccagggt cagctgcagc agtctggggc tgagctgggtg 780
aggcctgggt cctcagtga gatttcctgc aaggcttctg gctatgcatt cagtagctac 840
tggatgaact gggatgaagca gaggcctgga cagggtcttg agtggattgg acagatttgg 900
cctggagatg gtgatactaa ctacaatgga aagttcaagg gtaaagccac tctgactgca 960
gacgaatcct ccagcacagc ctacatgcaa ctcagcagcc tagcatctga ggactctgcg 1020
gtctatttct gtgcaagacg ggagactacg acggtaggcc gttattacta tgctatggac 1080

tactggggcc aaggaccac ggtcacgctc tcctccggtg gtggtggttc tggcggcggc 1140
 ggctccggtg gtggtggttc tgatatccag ctgacccagt ctccagcttc tttggctgtg 1200
 tctctagggc agagggccac catctcctgc aaggccagcc aaagtgttga ttatgatggt 1260
 gatagttatt tgaactggta ccaacagatt ccaggacagc cacccaaact cctcatctat 1320
 gatgcatcca atctagtttc tgggatccca cccaggttta gtggcagtgg gtctgggaca 1380
 gacttcaccc tcaacatcca tcctgtggag aaggtggatg ctgcaaccta tcaactgtcag 1440
 caaagtactg aggatccgtg gacgttcggt ggagggacca agctcgagat caaa 1494

<210> 327
 <211> 498
 <212> PRT
 <213> artificial sequence

<220>
 <223> VL1VH5xCD19 LHHL

<400> 327

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
 20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
 35 40 45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
 85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
 100 105 110

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
 115 120 125

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
 130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
 145 150 155 160

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
 165 170 175

Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe
 180 185 190

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
 195 200 205

Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr
 210 215 220

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
 225 230 235 240

Val Ser Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly
 245 250 255

Ala Glu Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala
 260 265 270

Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg
 275 280 285

Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly
 290 295 300

Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala
 305 310 315 320

Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser
 325 330 335

Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val
 340 345 350

Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val
 355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly

370

375

380

Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val
385 390 395 400

Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val
405 410 415

Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly
420 425 430

Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly
435 440 445

Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
450 455 460

Asn Ile His Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln
465 470 475 480

Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu
485 490 495

Ile Lys

<210> 328
<211> 1497
<212> DNA
<213> artificial sequence

<220>
<223> VH5VL1xCD19 HLHL

<400> 328
gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaagggtg 60
tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 120
cctggacagg gtctggaatg gattggatac attaataccta gccgtgggtta tactaattac 180
gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 240
atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300
gatgatcatt actgccttga ctactggggc caaggcacca cggtcacctg ctcctcaggc 360
gaaggtaacta gtactgggtc tgggtggaagt ggaggttcag gtggagcaga cgacattcag 420
atgacccagt ctccatctag cctgtctgca tctgtcgggg accgtgtcac catcacctgc 480

```

agagccagtc aaagtgtaag ttacatgaac tgggtaccagc agaagccggg caaggcaccc 540
aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaagggtg 720
gagatcaaat ccggagggtg tggatcccag gtgcagctgc agcagtctgg ggctgagctg 780
gtgaggcctg ggtcctcagt gaagatttcc tgcaaggctt ctggctatgc attcagtagc 840
tactggatga actgggtgaa gcagaggcct ggacagggtc ttgagtggat tggacagatt 900
tggcctggag atggtgatac taactacaat ggaaagttca agggtaaagc cactctgact 960
gcagacgaat cctccagcac agcctacatg caactcagca gcctagcatc tgaggactct 1020
gcggtctatt tctgtgcaag acgggagact acgacggtag gccgttatta ctatgctatg 1080
gactactggg gccaagggac cacggtcacc gtctcctccg gtgggtgggtg ttctggcggc 1140
ggcggctccg gtgggtgggtg ttctgatatc cagctgaccc agtctccagc ttctttggct 1200
gtgtctctag ggcagagggc caccatctcc tgcaaggcca gccaaagtgt tgattatgat 1260
ggtgatagtt atttgaactg gtaccaacag attccaggac agccacccaa actcctcatc 1320
tatgatgcat ccaatctagt ttctgggatc ccacccagggt ttagtggcag tgggtctggg 1380
acagacttca ccctcaacat ccctcctgtg gagaagggtg atgctgcaac ctatcactgt 1440
cagcaaagta ctgaggatcc gtggacgttc ggtggaggga ccaagctcga gatcaaa 1497

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<210> 329

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> VH5VL1xCD19 HLHL

<400> 329

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Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1           5           10           15

```

```

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20           25           30

```

```

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35           40           45

```

```

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val

```

50

55

60

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser
130 135 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser
245 250 255

Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys
260 265 270

Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln
275 280 285

Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp
290 295 300

Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr
305 310 315 320

Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala
325 330 335

Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr
340 345 350

Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr
355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
370 375 380

Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala
385 390 395 400

Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser
405 410 415

Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro
420 425 430

Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser
435 440 445

Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
450 455 460

Leu Asn Ile His Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys
465 470 475 480

Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu
485 490 495

Glu Ile Lys

<210> 330
<211> 1494
<212> DNA

<213> artificial sequence

<220>

<223> VL1VH5xCD19 LHLH

<400> 330

gacattcaga tgacccagtc tccatctagc ctgtctgcat ctgtcgggga ccgtgtcacc	60
atcacctgca gagccagtca aagtgttaagt tacatgaact ggtaccagca gaagccgggc	120
aaggcaccca aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctcgc	180
ttcagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa	240
gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cgggtggcggg	300
accaaggtgg agatcaaagg cgaaggtact agtactgggt ctgggtggaag tggaggttca	360
gggtggagcag acgacgtcca actgggtgcag tcaggggctg aagtgaaaaa acctggggcc	420
tcagtgaagg tgtcctgcaa ggcttctggc tacaccttta ctaggtacac gatgcactgg	480
gtaaggcagg cacctggaca ggtctctggaa tggattggat acattaatcc tagccgtggt	540
tatactaatt acgcagacag cgtcaagggc cgcttcacia tcactacaga caaatccacc	600
agcacagcct acatggaact gagcagcctg cgttctgagg aactgcaac ctattactgt	660
gcaagatatt atgatgatca ttactgcctt gactactggg gccaaggcac cacggtcacc	720
gtctcctccg gaggtgggtgg atccgatatc cagctgacct agtctccagc ttctttggct	780
gtgtctctag ggcagagggc caccatctcc tgcaaggcca gccaaagtgt tgattatgat	840
ggatgatagtt atttgaactg gtaccaacag attccaggac agccacccaa actcctcatc	900
tatgatgcat ccaatctagt ttctgggatc ccacccaggt ttagtggcag tgggtctggg	960
acagacttca ccctcaacat ccacctctgt gagaaggtgg atgctgcaac ctatcactgt	1020
cagcaaagta ctgaggatcc gtggacgttc ggtggaggga ccaagctcga gatcaaaggt	1080
gggtgggtggt ctggcggcgg cggtccgggt ggtgggtggt ctcagggtgca gctgcagcag	1140
tctggggctg agctgggtgag gcctgggtcc tcagtgaaga tttcctgcaa ggcttctggc	1200
tatgcattca gtagctactg gatgaactgg gtgaagcaga ggctggaca gggctcttgag	1260
tggattggac agatttggcc tggagatggg gatactaact acaatggaaa gttcaagggt	1320
aaagccactc tgactgcaga cgaatcctcc agcacagcct acatgcaact cagcagccta	1380
gcatctgagg actctgcggg ctatttctgt gcaagacggg agactacgac ggtaggccgt	1440
tattactatg ctatggacta ctggggccaa gggaccacgg tcaccgtctc ctcc	1494

<210> 331

<211> 498

<212> PRT

<213> artificial sequence

<220>

<223> VL1VH5xCD19 LHLH

<400> 331

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
100 105 110

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
115 120 125

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
145 150 155 160

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
165 170 175

Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe
180 185 190

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
195 200 205

Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr
210 215 220

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
225 230 235 240

Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro
245 250 255

Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys
260 265 270

Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr
275 280 285

Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser
290 295 300

Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly
305 310 315 320

Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val Asp Ala Ala
325 330 335

Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly
340 345 350

Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly
355 360 365

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu
370 375 380

Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly
385 390 395 400

Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly
405 410 415

Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr
420 425 430

Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu
435 440 445

Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu Asp
 450 455 460

Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val Gly Arg
 465 470 475 480

Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
 485 490 495

Ser Ser

<210> 332
 <211> 1497
 <212> DNA
 <213> artificial sequence

<220>
 <223> VH5VL1xCD19 HLLH

<400> 332
 gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctgggggcctc agtgaagggtg 60
 tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 120
 cctggacagg gtctggaatg gattggatac attaatccta gccgtgggtta tactaattac 180
 gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 240
 atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300
 gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc 360
 gaagg tacta gtactgggtc tgggtggaagt ggaggttcag gtggagcaga cgacattcag 420
 atgaccagtc ctccatctag cctgtctgca tctgtcgggg accgtgtcac catcacctgc 480
 agagccagtc aaagtgtaag ttacatgaac tgggtaccagc agaagccggg caaggcaccc 540
 aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
 agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
 acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaagggtg 720
 gagatcaa at ccggagggtg tggatccgat atccagctga ccagtcctcc agcttctttg 780
 gctgtgtctc tagggcagag ggccaccatc tcctgcaagg ccagccaaag tggtgattat 840
 gatggtgata gttatttgaa ctggtaccaa cagattccag gacagccacc caaactctc 900
 atctatgatg catccaatct agtttctggg atcccacca gggttagtgg cagtgggtct 960

```

gggacagact tcaccctcaa catccatcct gtggagaagg tggatgctgc aacctatcac 1020
tgtcagcaaa gtactgagga tccgtggacg ttcggtggag ggaccaagct cgagatcaaa 1080
ggtggtggtg gttctggcgg cggcggctcc ggtggtggtg gttctcaggt gcagctgcag 1140
cagtctgggg ctgagctggt gaggcctggg tcctcagtga agatttcctg caaggcttct 1200
ggctatgcat tcagtagcta ctggatgaac tgggtgaagc agaggcctgg acagggctct 1260
gagtggattg gacagatttg gcctggagat ggtgatacta actacaatgg aaagttcaag 1320
ggtaaagcca ctctgactgc agacgaatcc tccagcacag cctacatgca actcagcagc 1380
ctagcatctg aggactctgc ggtctatttc tgtgcaagac gggagactac gacggtaggc 1440
cgttattact atgctatgga ctactggggc caagggacca cggtcacctg ctctcc 1497

```

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<210> 333
<211> 499
<212> PRT
<213> artificial sequence

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<220>
<223> VH5VL1xCD19 HLLH

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<400> 333

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```

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1          5          10          15

```

```

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20          25          30

```

```

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35          40          45

```

```

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
50          55          60

```

```

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
65          70          75          80

```

```

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
85          90          95

```

```

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100          105          110

```

```

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115          120          125

```

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser
130 135 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser
245 250 255

Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys
260 265 270

Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp
275 280 285

Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala
290 295 300

Ser Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser
305 310 315 320

Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val Asp Ala
325 330 335

Ala Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly
340 345 350

Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly

355

360

365

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Ala
370 375 380

Glu Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser
385 390 395 400

Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro
405 410 415

Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly Asp
420 425 430

Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp
435 440 445

Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu
450 455 460

Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val Gly
465 470 475 480

Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
485 490 495

Val Ser Ser

<210> 334

<211> 1494

<212> DNA

<213> artificial sequence

<220>

<223> VL2/VH5xCD19 LHHL

<400> 334

gacattgtac tgaccagtc tccagcaact ctgtctctgt ctccagggga gcgtgccacc 60
ctgagctgca gagccagtca aagtgttaagt tacatgaact ggtaccagca gaagccgggc 120
aaggcaccca aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctcgc 180
ttcagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa 240
gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cggtggcggg 300
accaaggtgg agatcaaagg cgaaggtact agtactgggt ctggtggaag tggaggttca 360

ggtggagcag acgacgtcca actggtgcag tcaggggctg aagtgaaaaa acctggggcc 420
tcagtgaagg tgcctgcaa ggcttctggc tacaccttta ctaggtacac gatgcactgg 480
gtaaggcagg cacctggaca gggctctggaa tggattggat acattaatcc tagccgtggt 540
tatactaatt acgcagacag cgtcaagggc cgcttcacaa tcactacaga caaatccacc 600
agcacagcct acatggaact gagcagcctg cgttctgagg aactgcaac ctattactgt 660
gcaagatatt atgatgatca ttactgcctt gactactggg gccaaaggcac cacggtcacc 720
gtctcctccg gaggtggtgg atcccagggtg cagctgcagc agtctggggc tgagctggtg 780
aggcctgggt cctcagtga gatttcctgc aaggcttctg gctatgcatt cagtagctac 840
tggatgaact gggatgaagca gaggcctgga cagggtcttg agtggattgg acagatttgg 900
cctggagatg gtgatactaa ctacaatgga aagttcaagg gtaaagccac tctgactgca 960
gacgaatcct ccagcacagc ctacatgcaa ctcagcagcc tagcatctga ggactctgcg 1020
gtctatttct gtgcaagacg ggagactacg acggtaggcc gttattacta tgctatggac 1080
tactggggcc aagggaccac ggtcaccgtc tcctccggtg gtggtggttc tggcggcggc 1140
ggctccggtg gtggtggttc tgatatccag ctgaccagc ctccagcttc tttggctgtg 1200
tctctagggc agagggccac catctcctgc aaggccagcc aaagtgttga ttatgatggt 1260
gatagttatt tgaactggta ccaacagatt ccaggacagc caccctaaact cctcatctat 1320
gatgcatcca atctagtttc tgggatccca cccaggttta gtggcagtgg gtctgggaca 1380
gacttcaccc tcaacatcca tcctgtggag aagggtggatg ctgcaaccta tcactgtcag 1440
caaagtactg aggatccgtg gacgttcggt ggagggacca agctcgagat caaa 1494

<210> 335

<211> 498

<212> PRT

<213> artificial sequence

<220>

<223> VL2/VH5xCD19 LHHL

<400> 335

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr

35

40

45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
100 105 110

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
115 120 125

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
145 150 155 160

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
165 170 175

Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe
180 185 190

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
195 200 205

Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr
210 215 220

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
225 230 235 240

Val Ser Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly
245 250 255

Ala Glu Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala
260 265 270

Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg
275 280 285

Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly
290 295 300

Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala
305 310 315 320

Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser
325 330 335

Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val
340 345 350

Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val
355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val
385 390 395 400

Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val
405 410 415

Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly
420 425 430

Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly
435 440 445

Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
450 455 460

Asn Ile His Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln
465 470 475 480

Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu
485 490 495

Ile Lys

<210> 336
<211> 1497
<212> DNA
<213> artificial sequence

<220>
<223> VH5VL2xCD19 HLHL

<400> 336
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cctggacagg gtctggaatg gattggatac attaataccta gccgtgggta tactaattac 180
gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 240
atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc 360
gaaggtacta gtactgggtc tgggtggaagt ggaggttcag gtggagcaga cgacattgta 420
ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc 480
agagccagtc aaagtgtgaa ttacatgaac tgggtaccagc agaagccggg caaggcaccc 540
aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaaggtg 720
gagatcaaat ccggaggtgg tggatcccag gtgcagctgc agcagtctgg ggctgagctg 780
gtgaggcctg ggtcctcagt gaagatttcc tgcaaggctt ctggctatgc attcagtagc 840
tactggatga actgggtgaa gcagaggcct ggacagggtc ttgagtggat tggacagatt 900
tggcctggag atggtgatac taactacaat ggaaagttca agggtaaagc cactctgact 960
gcagacgaat cctccagcac agcctacatg caactcagca gcctagcatc tgaggactct 1020
gcggtctatt tctgtgcaag acgggagact acgacggtag gccgttatta ctatgctatg 1080
gactactggg gccaagggac cacggtcacc gtctcctccg gtgggtgggtg ttctggcggc 1140
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gtgtctctag ggcagagggc caccatctcc tgcaaggcca gccaaagtgt tgattatgat 1260
ggatgatagt atttgaactg gtaccaacag attccaggac agccacccaa actcctcatc 1320
tatgatgcat ccaatctagt ttctgggatc ccacccagggt ttagtggcag tgggtctggg 1380
acagacttca ccctcaacat ccatcctgtg gagaaggtgg atgctgcaac ctatcactgt 1440
cagcaaagta ctgaggatcc gtggacgttc ggtggaggga ccaagctcga gatcaaa 1497

<210> 337
<211> 499
<212> PRT
<213> artificial sequence

<220>
<223> VH5VL2xCD19 HLHL

<400> 337

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser
 245 250 255

Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys
 260 265 270

Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln
 275 280 285

Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp
 290 295 300

Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr
 305 310 315 320

Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala
 325 330 335

Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr
 340 345 350

Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr
 355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 370 375 380

Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala
 385 390 395 400

Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser
 405 410 415

Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro
 420 425 430

Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser
435 440 445

Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
450 455 460

Leu Asn Ile His Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys
465 470 475 480

Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu
485 490 495

Glu Ile Lys

<210> 338
<211> 1494
<212> DNA
<213> artificial sequence

<220>
<223> VL2/VH5xCD19

<400> 338
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ctgagctgca gagccagtca aagtgttaagt tacatgaact ggtaccagca gaagccgggc 120
aaggcaccca aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctcgc 180
ttcagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa 240
gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cggtggcggg 300
accaaggtgg agatcaaagg cgaaggtact agtactgggt ctggtggaag tggaggttca 360
ggtggagcag acgacgtcca actggtgcag tcaggggctg aagtgaaaaa acctggggcc 420
tcagtgaagg tgtcctgcaa ggcttctggc tacaccttta ctaggtacac gatgcactgg 480
gtaaggcagg cacctggaca ggtctctggaa tggattggat acattaatcc tagccgtggg 540
tatactaatt acgcagacag cgtcaagggc cgcttcacia tcaactacaga caaatccacc 600
agcacagcct acatggaact gagcagcctg cgttctgagg aactgcaac ctattactgt 660
gcaagatatt atgatgatca ttactgcctt gactactggg gccaaaggcac cacggtcacc 720
gtctcctccg gaggtgggtg atccgatatc cagctgaccc agtctccagc ttctttgggt 780
gtgtctctag ggcagagggc caccatctcc tgcaaggcca gccaaagtgt tgattatgat 840

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ggtgatagtt atttgaactg gtaccaacag attccaggac agccacccaa actcctcatc      900
tatgatgcat ccaatctagt ttctgggatc ccacccaggt ttagtggcag tgggtctggg      960
acagacttca ccctcaacat ccatacctgtg gagaagggtg atgctgcaac ctatcactgt     1020
cagcaaagta ctgaggatcc gtggacgttc ggtggaggga ccaagctcga gatcaaaggt     1080
ggtggtggtt ctggcggcgg cggctccggt ggtggtggtt ctcagggtgca gctgcagcag     1140
tctggggctg agctggtgag gcctgggtcc tcagtgaaga tttcctgcaa ggcttctggc     1200
tatgcattca gtagctactg gatgaactgg gtgaagcaga ggcctggaca gggctcttgag     1260
tggattggac agatttggcc tggagatggt gatactaact acaatggaaa gttcaagggt     1320
aaagccactc tgactgcaga cgaatcctcc agcacagcct acatgcaact cagcagccta     1380
gcatctgagg actctgcggt ctatttctgt gcaagacggg agactacgac ggtaggccgt     1440
tattactatg ctatggacta ctggggccaa gggaccacgg tcaccgtctc ctcc           1494

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<210> 339
<211> 498
<212> PRT
<213> artificial sequence

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<220>
<223> VL2/VH5xCD19

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```

<400> 339

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Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1           5           10           15

```

```

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
20           25           30

```

```

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
35           40           45

```

```

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50           55           60

```

```

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
65           70           75           80

```

```

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
85           90           95

```

```

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
100          105          110

```

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
 115 120 125
 Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
 130 135 140
 Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
 145 150 155 160
 Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
 165 170 175
 Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe
 180 185 190
 Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
 195 200 205
 Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr
 210 215 220
 Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
 225 230 235 240
 Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro
 245 250 255
 Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys
 260 265 270
 Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr
 275 280 285
 Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser
 290 295 300
 Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly
 305 310 315 320
 Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val Asp Ala Ala
 325 330 335
 Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly

340

345

350

Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly
 355 360 365

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu
 370 375 380

Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly
 385 390 395 400

Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly
 405 410 415

Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr
 420 425 430

Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu
 435 440 445

Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu Asp
 450 455 460

Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val Gly Arg
 465 470 475 480

Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
 485 490 495

Ser Ser

<210> 340
 <211> 1497
 <212> DNA
 <213> artificial sequence

<220>
 <223> VH5VL2xCD19 HLLH

<400> 340
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 cctggacagg gtctggaatg gattggatac attaataccta gccgtgggta tactaattac 180
 gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 240

atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300
 gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctccctcaggc 360
 gaagggtacta gtactgggttc tgggtggaagt ggaggttcag gtggagcaga cgacattgta 420
 ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc 480
 agagccagtc aaagtgtgtaag ttacatgaac tgggtaccagc agaagccggg caaggcaccc 540
 aaaagatgga tttatgacac atccaaagtg gcttctggag tccttgctcg cttcagtggc 600
 agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
 acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaagggtg 720
 gagatcaaat ccggagggtg tggatccgat atccagctga ccagctctcc agcttctttg 780
 gctgtgtctc tagggcagag ggccaccatc tcctgcaagg ccagccaaag tggttgattat 840
 gatggtgata gttatttgaa ctggtaccaa cagattccag gacagccacc caaactcctc 900
 atctatgatg catccaatct agtttctggg atcccacca ggtttagtgg cagtgggtct 960
 gggacagact tcacctcaa catccatcct gtggagaagg tggatgctgc aacctatcac 1020
 tgtcagcaaa gtactgagga tccgtggacg ttcggtggag ggaccaagct cgagatcaaa 1080
 ggtggtggtg gttctggcgg cggcggtctc ggtggtggtg gttctcaggt gcagctgcag 1140
 cagtctgggg ctgagctggt gaggcctggg tcctcagtga agatttcctg caaggcttct 1200
 ggctatgcat tcagtagcta ctggatgaac tgggtgaagc agaggcctgg acagggtctt 1260
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 ggtaaagcca ctctgactgc agacgaatcc tccagcacag cctacatgca actcagcagc 1380
 ctagcatctg aggactctgc ggtctatttc tgtgcaagac gggagactac gacggtaggc 1440
 cgttattact atgctatgga ctactggggc caagggacca cggtcaccgt ctccctcc 1497

<210> 341

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> VH5VL2xCD19 HLLH

<400> 341

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr

20

25

30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
 85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
 115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
 130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
 145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser
 245 250 255

Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys
 260 265 270

Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp
 275 280 285

Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala
 290 295 300

Ser Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser
 305 310 315 320

Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val Asp Ala
 325 330 335

Ala Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly
 340 345 350

Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly
 355 360 365

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Ala
 370 375 380

Glu Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser
 385 390 395 400

Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro
 405 410 415

Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly Asp
 420 425 430

Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp
 435 440 445

Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu
 450 455 460

Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val Gly
 465 470 475 480

Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
 485 490 495

Val Ser Ser

<210> 342
<211> 1494
<212> DNA
<213> artificial sequence

<220>
<223> VL3VH5xCD19 LHHL

<400> 342
gacattgtac tgacccagtc tccagcaact ctgtctctgt ctccagggga gcgtgccacc 60
ctgacctgca gagccagttc aagtgttaagt tacatgaact ggtaccagca gaagccgggc 120
aaggcaccca aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctcgc 180
ttcagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa 240
gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cgggtggcggg 300
accaaggtgg agatcaaagg cgaagggtact agtactgggt ctggtggaag tggagggttca 360
ggtggagcag acgacgtcca actggtgcag tcaggggctg aagtgaaaaa acctggggcc 420
tcagtgaagg tgcctgcaa ggcttctggc tacaccttta ctaggtacac gatgcactgg 480
gtaaggcagg cacctggaca gggctctggaa tggattggat acattaatcc tagccgtggg 540
tatactaatt acgcagacag cgtcaagggc cgcttcacia tcactacaga caaatccacc 600
agcacagcct acatggaact gagcagcctg cgcttctgagg aactgcaac ctattactgt 660
gcaagatatt atgatgatca ttactgcctt gactactggg gccaaaggcac cacggtcacc 720
gtctcctccg gaggtgggtg atcccagggtg cagctgcagc agtctggggc tgagctgggtg 780
aggcctgggt cctcagtga gatttcctgc aaggcttctg gctatgcatt cagtagctac 840
tggatgaact ggggtgaagca gaggcctgga cagggctctg agtggattgg acagatttgg 900
cctggagatg gtgatactaa ctacaatgga aagttcaagg gtaaagccac tctgactgca 960
gacgaatcct ccagcacagc ctacatgcaa ctacagagcc tagcatctga ggactctgcg 1020
gtctatttct gtgcaagacg ggagactacg acggtaggcc gttattacta tgctatggac 1080
tactggggcc aagggaccac gggtcacctg tctccgggtg gtgggtgggtc tggcggcggc 1140
ggctccgggtg gtgggtgggtc tgatatccag ctgacccagt ctccagcttc tttggctgtg 1200
tctctagggc agagggccac catctcctgc aaggccagcc aaagtgttga ttatgatggg 1260
gatagttatt tgaactggta ccaacagatt ccaggacagc caccctaaact cctcatctat 1320
gatgcacca atctagtttc tgggatccca ccaggttta gtggcagtgg gtctgggaca 1380

gacttcaccc tcaacatcca tcctgtggag aaggtggatg ctgcaaccta tcactgtcag 1440
caaagtactg aggatccgtg gacgttcggt ggagggacca agctcgagat caaa 1494

<210> 343
<211> 498
<212> PRT
<213> artificial sequence

<220>
<223> VL3VH5xCD19 LHHL

<400> 343

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
100 105 110

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
115 120 125

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
145 150 155 160

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
165 170 175

Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe
180 185 190

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
195 200 205

Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr
210 215 220

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
225 230 235 240

Val Ser Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly
245 250 255

Ala Glu Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala
260 265 270

Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg
275 280 285

Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly
290 295 300

Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala
305 310 315 320

Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser
325 330 335

Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val
340 345 350

Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val
355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val
385 390 395 400

Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val
405 410 415

Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly
 420 425 430

Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly
 435 440 445

Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
 450 455 460

Asn Ile His Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln
 465 470 475 480

Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu
 485 490 495

Ile Lys

<210> 344
 <211> 1497
 <212> DNA
 <213> artificial sequence

<220>
 <223> VH5VL3xCD19 HLHL

<400> 344
 gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaagggtg 60
 tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 120
 cctggacagg gtctggaatg gattggatac attaataccta gccgtgggtta tactaattac 180
 gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 240
 atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300
 gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc 360
 gaaggtaacta gtactgggttc tgggtggaagt ggaggttcag gtggagcaga cgacattgta 420
 ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgacctgc 480
 agagccagtt caagtgtaag ttacatgaac tgggtaccagc agaagccggg caaggcaccc 540
 aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
 agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
 acttattact gccaacagtg gagtagtaac ccgctcacgt tcgggtggcgg gaccaagggtg 720

gagatcaa at ccggaggtgg tggatcccag gtgcagctgc agcagtctgg ggctgagctg 780
 gtgaggcctg ggtcctcagt gaagatttcc tgcaaggcct ctggctatgc attcagtagc 840
 tactggatga actgggtgaa gcagaggcct ggacagggtc ttgagtggat tggacagatt 900
 tggcctggag atggtgatac taactacaat ggaaagtica agggtaaagc cactctgact 960
 gcagacgaat cctccagcac agcctacatg caactcagca gcctagcatc tgaggactct 1020
 gcggtctatt tctgtgcaag acgggagact acgacggtag gccgttatta ctatgctatg 1080
 gactactggg gccaaaggac cacggtcacc gtctcctccg gtggtgggtg ttctggcggc 1140
 ggcggctccg gtggtgggtg ttctgatatc cagctgaccc agtctccagc ttctttggct 1200
 gtgtctctag ggcagagggc caccatctcc tgcaaggcca gccaaagtgt tgattatgat 1260
 ggtgatagtt atttgaactg gtaccaacag attccaggac agccacccaa actcctcatc 1320
 tatgatgcat ccaatctagt ttctgggatc ccacccaggt ttagtggcag tgggtctggg 1380
 acagacttica ccctcaacat ccatcctgtg gagaagggtg atgctgcaac ctatcactgt 1440
 cagcaaagta ctgaggatcc gtggacgttc ggtggaggga ccaagctcga gatcaaa 1497

<210> 345

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> VH5VL3xCD19 HLHL

<400> 345

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
 85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys
145 150 155 160

Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser
245 250 255

Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys
260 265 270

Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln
275 280 285

Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp
290 295 300

Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr
305 310 315 320

Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala

325

330

335

Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr
340 345 350

Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr
355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
370 375 380

Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala
385 390 395 400

Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser
405 410 415

Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro
420 425 430

Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser
435 440 445

Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
450 455 460

Leu Asn Ile His Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys
465 470 475 480

Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu
485 490 495

Glu Ile Lys

<210> 346
<211> 1494
<212> DNA
<213> artificial sequence

<220>
<223> VL3VH5xCD19 LHLH

<400> 346
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aaggcacc ca aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctcgc 180
ttcagtgg ca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa 240
gatgctgc ca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cgggtggcggg 300
accaaggtgg agatcaaagg cgaaggtact agtactgggt ctggtggaag tggaggttca 360
ggtggagcag acgacgtcca actggtgcag tcaggggctg aagtgaaaaa acctggggcc 420
tcagtgaagg tgtcctgcaa ggcttctggc tacaccttta ctaggtacac gatgcactgg 480
gtaaggcagg cacctggaca gggctctggaa tggattggat acattaatcc tagccgtggg 540
tatactaatt acgcagacag cgtcaagggc cgcttcacia tcactacaga caaatccacc 600
agcacagcct acatggaact gagcagcctg cgttctgagg aactgcaac ctattactgt 660
gcaagatatt atgatgatca ttactgcctt gactactggg gccaaaggcac cacggtcacc 720
gtctcctccg gaggtgggtg atccgatatc cagctgacct agtctccagc ttctttggct 780
gtgtctctag ggcagagggc caccatctcc tgcaaggcca gccaaagtgt tgattatgat 840
ggtgatagtt atttgaactg gtaccaacag attccaggac agccacccaa actcctcatc 900
tatgatgcat ccaatctagt ttctgggatc ccacccaggt ttagtggcag tgggtctggg 960
acagacttca ccctcaacat ccctcctgtg gagaaggtgg atgctgcaac ctatcactgt 1020
cagcaaagta ctgaggatcc gtggacgttc ggtggaggga ccaagctcga gatcaaaggt 1080
ggtggtgggt ctggcggcgg cggctccggt ggtggtgggt ctcagggtga gctgcagcag 1140
tctggggctg agctgggtgag gcctgggtcc tcagtgaaga tttcctgcaa ggcttctggc 1200
tatgcattca gtagctactg gatgaactgg gtgaagcaga ggcctggaca gggctctgag 1260
tggattggac agatttggcc tggagatggt gatactaact acaatggaaa gttcaagggt 1320
aaagccactc tgactgcaga cgaatcctcc agcacagcct acatgcaact cagcagccta 1380
gcactgagg actctgcggt ctatttctgt gcaagacggg agactacgac ggtaggccgt 1440
tattactatg ctatggacta ctggggccaa gggaccacgg tcaccgtctc ctcc 1494

<210> 347

<211> 498

<212> PRT

<213> artificial sequence

<220>

<223> VL3VH5xCD19 LHLH

<400> 347

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly

1	5	10	15
Glu Arg Ala Thr Leu Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met	20	25	30
Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr	35	40	45
Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser	50	55	60
Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu	65	70	75
Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr	85	90	95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr	100	105	110
Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu	115	120	125
Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val	130	135	140
Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp	145	150	155
Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn	165	170	175
Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe	180	185	190
Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser	195	200	205
Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr	210	215	220
Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr	225	230	235
			240

Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro.
245 250 255

Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys
260 265 270

Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr
275 280 285

Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser
290 295 300

Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly
305 310 315 320

Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val Asp Ala Ala
325 330 335

Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly
340 345 350

Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly
355 360 365

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu
370 375 380

Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly
385 390 395 400

Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly
405 410 415

Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr
420 425 430

Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu
435 440 445

Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu Asp
450 455 460

Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val Gly Arg
465 470 475 480

Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
485 490 495

Ser Ser

<210> 348
<211> 1497
<212> DNA
<213> artificial sequence

<220>
<223> VH5VL3xCD19 HLLH

<400> 348
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tcttgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 120
cctggacagg gtctggaatg gattggatac attaatecta gccgtgggtta tactaattac 180
gcagacagcg tcaagggccg cttcacatc actacagaca aatccaccag cacagcctac 240
atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc 360
gaaggtaacta gtactgggtc tgggtggaagt ggagggttcag gtggagcaga cgacattgta 420
ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgacctgc 480
agagccagtt caagtgtgtaag ttacatgaac tgggtaccagc agaagccggg caaggcaccc 540
aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcgggtggcgg gaccaagggtg 720
gagatcaaatt ccggagggtg tggatccgat atccagctga ccagctctcc agcttctttg 780
gctgtgtctc tagggcagag ggccaccatc tcttgcaagg ccagccaaag tggtgattat 840
gatggtgata gttatttgaa ctggtaccaa cagattccag gacagccacc caaactcctc 900
atctatgatg catccaatct agtttctggg atcccacca ggtttagtgg cagtgggtct 960
gggacagact tcaccctcaa catccatcct gtggagaagg tggatgctgc aacctatcac 1020
tgtcagcaaa gtactgagga tccgtggacg ttcggtggag ggaccaagct cgagatcaaa 1080
ggtgggtggtg gttctggcgg cggcggctcc ggtgggtggtg gttctcagggt gcagctgcag 1140
cagtctgggg ctgagctggt gaggcctggg tcctcagtga agatttcctg caaggcttct 1200
ggctatgcat tcagtagcta ctggatgaac tgggtgaagc agaggcctgg acagggtctt 1260

gagtggattg gacagatttg gcctggagat ggtgatacta actacaatgg aaagttcaag 1320
 ggtaaagcca ctctgactgc agacgaatcc tccagcacag cctacatgca actcagcagc 1380
 ctagcatctg aggactctgc ggtctatttc tgtgcaagac gggagactac gacggtaggc 1440
 cgttattact atgctatgga ctactggggc caagggacca cggtcacccgt ctcctcc 1497

<210> 349
 <211> 499
 <212> PRT
 <213> artificial sequence

<220>
 <223> VH5VL3xCD19 HLLH

<400> 349

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
 85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
 115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
 130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys
 145 150 155 160

Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser
245 250 255

Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys
260 265 270

Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp
275 280 285

Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala
290 295 300

Ser Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser
305 310 315 320

Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val Asp Ala
325 330 335

Ala Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly
340 345 350

Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly
355 360 365

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Ala
370 375 380

Glu Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser
385 390 395 400

Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro
405 410 415

Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly Asp
420 425 430

Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp
435 440 445

Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu
450 455 460

Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val Gly
465 470 475 480

Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
485 490 495

Val Ser Ser

<210> 350
<211> 1494
<212> DNA
<213> artificial sequence

<220>
<223> VL1VH7xCD19 LHHL

<400> 350
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aaggcaccga aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctcgc 180
ttcagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa 240
gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cggtggcggg 300
accaaggtgg agatcaaagg cgaaggtact agtactgggt ctggtggaag tggaggttca 360
ggtggagcag acgacgtcca actggtgcag tcaggggctg aagtgaaaaa acctggggcc 420
tcagtgaagg tgtcctgcaa ggcttctggc tacaccttta ctaggtacac gatgcactgg 480
gtaaggcagg cacctggaca gggctctggaa tggattggat acattaatcc tagccgtggg 540
tatactaatt acaatcagaa gttcaaggac cgcgtcacia tcaactacaga caaatccacc 600

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agcacagcct acatggaact gagcagcctg cgttctgagg aactgcagt ctattactgt      660
gcaagatatt atgatgatca ttactgcctt gactactggg gccaaaggcac cacggtcacc      720
gtctcctccg gaggtggtgg atcccagggtg cagctgcagc agtctggggc tgagctggtg      780
aggcctgggt cctcagtga gatttcctgc aaggcttctg gctatgcatt cagtagctac      840
tggatgaact gggatgaagca gaggcctgga cagggtcttg agtggattgg acagatttgg      900
cctggagatg gtgatactaa ctacaatgga aagttcaagg gtaaagccac tctgactgca      960
gacgaatcct ccagcacagc ctacatgcaa ctcagcagcc tagcatctga ggactctgcg     1020
gtctatcttct gtgcaagacg ggagactacg acggtaggcc gttattacta tgctatggac     1080
tactggggcc aagggaccac ggtcaccgtc tcctccggtg gtggtggttc tggcggcggc     1140
ggctccggtg gtggtggttc tgatatccag ctgaccagc ctccagcttc tttggctgtg     1200
tctctagggc agagggccac catctcctgc aaggccagcc aaagtgttga ttatgatggt     1260
gatagttatt tgaactggta ccaacagatt ccaggacagc cacccaaact cctcatctat     1320
gatgcatcca atctagtttc tgggatccca cccaggttta gtggcagtgg gtctgggaca     1380
gacttcaccc tcaacatcca tcctgtggag aaggtggatg ctgcaaccta tcaactgtcag     1440
caaagtactg aggatccgtg gacgttcggt ggagggacca agctcgagat caaa          1494

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<210> 351

<211> 498

<212> PRT

<213> artificial sequence

<220>

<223> VL1VH7xCD19 LHHL

<400> 351

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1           5           10           15

```

```

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
20           25           30

```

```

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
35           40           45

```

```

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50           55           60

```

```

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
65           70           75           80

```

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
100 105 110

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
115 120 125

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
145 150 155 160

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
165 170 175

Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
180 185 190

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
195 200 205

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr
210 215 220

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
225 230 235 240

Val Ser Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly
245 250 255

Ala Glu Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala
260 265 270

Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg
275 280 285

Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly
290 295 300

Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala

305 310 315 320

Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser
 325 330 335

Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val
 340 345 350

Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val
 355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 370 375 380

Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val
385 390 395 400

Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val
 405 410 415

Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly
 420 425 430

Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly
 435 440 445

Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
450 455 460

Asn Ile His Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln
465 470 475 480

Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu
 485 490 495

Ile Lys

<210> 352
<211> 1497
<212> DNA
<213> artificial sequence

<220>
<223> VH7VL1xCD19 HLHL

<400> 352

gacgtccaac	tggtgcagtc	aggggctgaa	gtgaaaaaac	ctggggcctc	agtgaagggtg	60
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cctggacagg	gtctggaatg	gattggatac	attaatccta	gccgtgggta	tactaattac	180
aatcagaagt	tcaaggaccg	cgtcacaatc	actacagaca	aatccaccag	cacagcctac	240
atggaactga	gcagcctgcg	ttctgaggac	actgcagtct	attactgtgc	aagatattat	300
gatgatcatt	actgccttga	ctactggggc	caaggcacca	cggtcaccgt	ctcctcaggc	360
gaagg tacta	gtactggttc	tggtggaagt	ggagggttcag	gtggagcaga	cgacattcag	420
atgacccagt	ctccatctag	cctgtctgca	tctgtcgggg	accgtgtcac	catcacctgc	480
agagccagtc	aaagtgt aag	ttacatgaac	tggtaccagc	agaagccggg	caaggcaccc	540
aaaagatgga	tttatgacac	atccaaagtg	gcttctggag	tccttgctcg	cttcagtggc	600
agtgggtctg	ggaccgacta	ctctctcaca	atcaacagct	tggaggctga	agatgctgcc	660
acttattact	gccaacagtg	gagtagtaac	ccgctcacgt	tcgggtggcg	gaccaagggtg	720
gagatcaa at	ccggagggtg	tggatcccag	gtgcagctgc	agcagtctgg	ggctgagctg	780
gtgaggcctg	ggtcctcagt	gaagatttcc	tgcaaggctt	ctggctatgc	attcagtagc	840
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tggcctggag	atggtgatac	taactacaat	ggaaagttca	agggtaaagc	cactctgact	960
gcagacgaat	cctccagcac	agcctacatg	caactcagca	gcctagcatc	tgaggactct	1020
gcggtctatt	tctgtgcaag	acgggagact	acgacggtag	gccgttatta	ctatgctatg	1080
gactactggg	gccaagggac	cacggtcacc	gtctcctccg	gtgggtgggtg	ttctggcggc	1140
ggcggctccg	gtgggtgggtg	ttctgatatc	cagctgacce	agtctccagc	ttctttggct	1200
gtgtctctag	ggcagagggc	caccatctcc	tgcaaggcca	gccaagtggt	tgattatgat	1260
ggtgatagtt	atttgaactg	gtaccaacag	attccaggac	agccacccaa	actcctcatc	1320
tatgatgcat	ccaatctagt	ttctgggatc	ccaccaggt	ttagtggcag	tgggtctggg	1380
acagacttca	ccctcaacat	ccatcctgtg	gagaagggtg	atgctgcaac	ctatcactgt	1440
cagcaaagta	ctgaggatcc	gtggacgttc	ggtggaggga	ccaagctcga	gatcaaaa	1497

<210> 353

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> VH7VL1xCD19 HLHL

<400> 353

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
 50 55 60

Lys Asp Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
 115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser
 130 135 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
 145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser
 245 250 255

Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys
 260 265 270

Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln
 275 280 285

Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp
 290 295 300

Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr
 305 310 315 320

Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala
 325 330 335

Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr
 340 345 350

Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr
 355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 370 375 380

Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala
 385 390 395 400

Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser
 405 410 415

Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro
 420 425 430

Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser
 435 440 445

Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 450 455 460

Leu Asn Ile His Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys
465 470 475 480

Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu
485 490 495

Glu Ile Lys

<210> 354
<211> 1494
<212> DNA
<213> artificial sequence

<220>
<223> VL1VH7xCD19 LHLH

<400> 354
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atcacctgca gagccagtca aagtgttaagt tacatgaact ggtaccagca gaagccgggc 120
aaggcaccga aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctcgc 180
ttcagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa 240
gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cggtggcggg 300
accaaggtgg agatcaaagg cgaaggtact agtactgggt ctggtggaag tggaggttca 360
ggtggagcag acgacgtcca actggtgcag tcaggggctg aagtgaaaaa acctggggcc 420
tcagtgaagg tgtcctgcaa ggcttctggc tacaccttta ctaggtacac gatgcactgg 480
gtaaggcagg cacctggaca gggctctggaa tggattggat acattaatcc tagccgtggg 540
tatactaatt acaatcagaa gttcaaggac cgcgtcacia tcactacaga caaatccacc 600
agcacagcct acatggaact gagcagcctg cggttctgagg aactgcagt ctattactgt 660
gcaagatatt atgatgatca ttactgcctt gactactggg gccaaaggcac cacggtcacc 720
gtctcctccg gaggtgggtg atccgatatc cagctgaccc agtctccagc ttctttggct 780
gtgtctctag ggcagagggc caccatctcc tgcaaggcca gccaaagtgt tgattatgat 840
ggtgatagtt atttgaactg gtaccaacag attccaggac agccacccaa actcctcatc 900
tatgatgcat ccaatctagt ttctgggatc ccaccaggt ttagtggcag tgggtctggg 960
acagacttca ccctcaacat ccatcctgtg gagaaggtgg atgctgcaac ctatcactgt 1020
cagcaaagta ctgaggatcc gtggacgttc ggtggaggga ccaagctcga gatcaaaggt 1080
ggtgggtggt ctggcggcgg cggtccggg ggtgggtggt ctcaggtgca gctgcagcag 1140

tctggggctg agctggtgag gcctgggtcc tcagtgaaga tttcctgcaa ggcttctggc 1200
tatgcattca gtagctactg gatgaactgg gtgaagcaga ggcctggaca gggctcttgag 1260
tggattggac agatttggcc tggagatggt gatactaact acaatggaaa gttcaagggg 1320
aaagccactc tgactgcaga cgaatcctcc agcacagcct acatgcaact cagcagccta 1380
gcatctgagg actctgcggt ctatttctgt gcaagacggg agactacgac ggtaggccgt 1440
tattactatg ctatggacta ctggggccaa gggaccacgg tcaccgtctc ctcc 1494

<210> 355

<211> 498

<212> PRT

<213> artificial sequence

<220>

<223> VL1VH7xCD19 LHLH

<400> 355

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
100 105 110

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
115 120 125

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
145 150 155 160

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
165 170 175

Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
180 185 190

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
195 200 205

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr
210 215 220

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
225 230 235 240

Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro
245 250 255

Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys
260 265 270

Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr
275 280 285

Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser
290 295 300

Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly
305 310 315 320

Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val Asp Ala Ala
325 330 335

Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly
340 345 350

Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly
355 360 365

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu
370 375 380

Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly
385 390 395 400

Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly
405 410 415

Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr
420 425 430

Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu
435 440 445

Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu Asp
450 455 460

Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val Gly Arg
465 470 475 480

Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
485 490 495

Ser Ser

<210> 356
<211> 1497
<212> DNA
<213> artificial sequence

<220>
<223> VH7VL1xCD19 HLLH

<400> 356
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tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 120
cctggacagg gtctggaatg gattggatac attaatccta gccgtgggtta tactaattac 180
aatcagaagt tcaaggaccg cgtcacaatc actacagaca aatccaccag cacagcctac 240
atggaactga gcagcctgcg ttctgaggac actgcagtct attactgtgc aagatattat 300
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc 360
gaaggtacta gtactgggtc tgggtggaagt ggaggttcag gtggagcaga cgacattcag 420
atgaccagat ctccatctag cctgtctgca tctgtcgggg accgtgtcac catcacctgc 480

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agagccagtc aaagtgtgtaag ttacatgaac tgggtaccagc agaagccggg caaggcaccc 540
aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaagggtg 720
gagatcaaat ccggagggtg tggatccgat atccagctga cccagtctcc agcttctttg 780
gctgtgtctc tagggcagag ggccaccatc tcctgcaagg ccagccaaag tgttgattat 840
gatgggtgata gttatttgaa ctggtaccaa cagattccag gacagccacc caaactcctc 900
atctatgatg catccaatct agtttctggg atcccaccca ggtttagtgg cagtgggtct 960
gggacagact tcaccctcaa catccatcct gtggagaagg tggatgctgc aacctatcac 1020
tgtcagcaaa gtactgagga tccgtggacg ttcggtggag ggaccaagct cgagatcaaa 1080
ggtggtggtg gttctggcgg cggcggctcc ggtggtggtg gttctcaggt gcagctgcag 1140
cagtctgggg ctgagctggt gaggcctggg tcctcagtga agatttcctg caaggcttct 1200
ggctatgcat tcagtāgcta ctggatgaac tgggtgaagc agaggcctgg acagggtctt 1260
gagtggattg gacagatttg gcctggagat ggtgatacta actacaatgg aaagttcaag 1320
ggtaaagcca ctctgactgc agacgaatcc tccagcacag cctacatgca actcagcagc 1380
ctagcatctg aggactctgc ggtctatttc tgtgcaagac gggagactac gacggtaggc 1440
cgttattact atgctatgga ctactggggc caagggacca cggtcaccgt ctcctcc 1497

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<210> 357

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> VH7VL1xCD19 HLLH

<400> 357

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Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1           5           10           15

```

```

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20           25           30

```

```

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35           40           45

```

```

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
50           55           60

```

Lys Asp Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser
130 135 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser
245 250 255

Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys
260 265 270

Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp
275 280 285

Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala

290

295

300

Ser Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser
305 310 315 320

Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val Asp Ala
325 330 335

Ala Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly
340 345 350

Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly
355 360 365

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Ala
370 375 380

Glu Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser
385 390 395 400

Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro
405 410 415

Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly Asp
420 425 430

Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp
435 440 445

Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu
450 455 460

Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val Gly
465 470 475 480

Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
485 490 495

Val Ser Ser

<210> 358

<211> 1494

<212> DNA

<213> artificial sequence

<220>

<223> VL2VH7xCD19 LHHL

<400> 358

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aaggcaccca aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctcgc	180
ttcagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa	240
gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cgggtggcggg	300
accaaggtgg agatcaaagg cgaaggtact agtactgggt ctggtggaag tggagggttca	360
ggtggagcag acgacgtcca actggtgcag tcaggggctg aagtgaaaaa acctggggcc	420
tcagtgaagg tgcctgcaa ggcttctggc tacaccttta ctaggtacac gatgcactgg	480
gtaaggcagg cacctggaca gggctctggaa tggattggat acattaatcc tagccgtggt	540
tatactaatt acaatcagaa gttcaaggac cgcgtcacia tcactacaga caaatccacc	600
agcacagcct acatggaact gagcagcctg cgttctgagg aactgcagt ctattactgt	660
gcaagatatt atgatgatca ttactgcctt gactactggg gccaaaggcac cacggtcacc	720
gtctcctccg gaggtggtgg atcccagggt cagctgcagc agtctggggc tgagctggtg	780
aggcctgggt cctcagtga gatttcctgc aaggcttctg gctatgcatt cagtagctac	840
tggatgaact ggggtgaagca gaggcctgga cagggctctg agtggattgg acagatttgg	900
cctggagatg gtgatactaa ctacaatgga aagttcaagg gtaaagccac tctgactgca	960
gacgaatcct ccagcacagc ctacatgcaa ctacagcagc tagcatctga ggactctgcg	1020
gtctatttct gtgcaagacg ggagactacg acggtaggcc gttattacta tgctatggac	1080
tactggggcc aagggaccac ggtcaccgtc tcctccgggtg gtggtggttc tggcggcggc	1140
ggctccgggtg gtggtggttc tgatatccag ctgacccagt ctccagcttc tttggctgtg	1200
tctctagggc agagggccac catctcctgc aaggccagcc aaagtgttga ttatgatggt	1260
gatagttatt tgaactggta ccaacagatt ccaggacagc caccctaaact cctcatctat	1320
gatgcacca atctagtttc tgggatccca cccagggtta gtggcagtgg gtctgggaca	1380
gacttcaccc tcaacatcca tcctgtggag aaggtggatg ctgcaaccta tcaactgtcag	1440
caaagtactg aggatccgtg gacgttcggt ggagggacca agctcgagat caaa	1494

<210> 359

<211> 498

<212> PRT

<213> artificial sequence

<220>

<223> VL2VH7xCD19 LHHL

<400> 359

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
100 105 110

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
115 120 125

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
145 150 155 160

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
165 170 175

Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
180 185 190

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
195 200 205

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr
 210 215 220

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
 225 230 235 240

Val Ser Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly
 245 250 255

Ala Glu Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala
 260 265 270

Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg
 275 280 285

Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly
 290 295 300

Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala
 305 310 315 320

Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser
 325 330 335

Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val
 340 345 350

Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val
 355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 370 375 380

Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val
 385 390 395 400

Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val
 405 410 415

Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly
 420 425 430

Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly
 435 440 445

Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
450 455 460

Asn Ile His Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln
465 470 475 480

Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu
485 490 495

Ile Lys

<210> 360
<211> 1497
<212> DNA
<213> artificial sequence

<220>
<223> VH7VL2xCD19 HLHL

<400> 360
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cctggacagg gtctggaatg gattggatac attaatacta gccgtgggtta tactaattac 180
aatcagaagt tcaaggaccg cgtcacaatc actacagaca aatccaccag cacagcctac 240
atggaactga gcagcctgcg ttctgaggac actgcagtct attactgtgc aagatattat 300
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc 360
gaagggtacta gtactgggttc tgggtggaagt ggaggttcag gtggagcaga cgacattgta 420
ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc 480
agagccagtc aaagtgtgtaag ttacatgaac tgggtaccagc agaagccggg caaggcaccc 540
aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcgggtggcgg gaccaagggtg 720
gagatcaaata ccggagggtg tggatcccag gtgcagctgc agcagtctgg ggctgagctg 780
gtgaggcctg ggtcctcagt gaagatttcc tgcaaggctt ctggctatgc attcagtagc 840
tactggatga actgggtgaa gcagaggcct ggacagggtc ttgagtggat tggacagatt 900
tggcctggag atgggtgatac taactacaat ggaaagttca agggtaaagc cactctgact 960
gcagacgaat cctccagcac agcctacatg caactcagca gcctagcatc tgaggactct 1020

gcggtctatt tctgtgcaag acgggagact acgacggtag gccgttatta ctatgctatg 1080
gactactggg gccaaaggac cacggtcacc gtctcctccg gtgggtgggtg ttctggcggc 1140
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gtgtctctag ggcagagggc caccatctcc tgcaaggcca gccaaagtgt tgattatgat 1260
ggtgatagtt atttgaactg gtaccaacag attccaggac agccacccaa actcctcatc 1320
tatgatgcat ccaatctagt ttctgggatc ccaccaggt ttagtggcag tgggtctggg 1380
acagacttca ccctcaacat ccatactgtg gagaagggtg atgctgcaac ctatcactgt 1440
cagcaaagta ctgaggatcc gtggacgttc ggtggaggga ccaagctcga gatcaaa 1497

<210> 361
<211> 499
<212> PRT
<213> artificial sequence

<220>
<223> VH7VL2xCD19 HLHL

<400> 361

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser
245 250 255

Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys
260 265 270

Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln
275 280 285

Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp
290 295 300

Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr
305 310 315 320

Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala
325 330 335

Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr
340 345 350

Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr
355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
370 375 380

Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala
385 390 395 400

Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser
405 410 415

Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro
420 425 430

Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser
435 440 445

Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
450 455 460

Leu Asn Ile His Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys
465 470 475 480

Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu
485 490 495

Glu Ile Lys

<210> 362
<211> 1494
<212> DNA
<213> artificial sequence

<220>
<223> VL2VH7xCD19 LHLH

<400> 362
gacattgtac tgaccagtc tccagcaact ctgtctctgt ctccagggga gcgtgccacc 60
ctgagctgca gagccagtca aagtgttaagt tacatgaact ggtaccagca gaagccgggc 120
aaggcaccga aaagatggat ttatgacaca tccaaagtgg cttctggagt cctgctcgc 180
ttcagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa 240
gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cggtggcggg 300
accaaggtgg agatcaaagg cgaaggtact agtactgggt ctggtggaag tggaggttca 360

ggtggagcag acgacgtcca actggtgcag tcaggggctg aagtgaaaaa acctgggggc 420
tcagtgaagg tgtcctgcaa ggcttctggc tacaccttta ctaggtacac gatgcactgg 480
gtaaggcagg cacctggaca gggctctggaa tggattggat acattaatcc tagccgtggt 540
tatactaatt acaatcagaa gttcaaggac cgcgtcacia tcactacaga caaatccacc 600
agcacagcct acatggaact gagcagcctg cgttctgagg aactgcagt ctattactgt 660
gcaagatatt atgatgatca ttactgcctt gactactggg gccaaaggcac cacggtcacc 720
gtctcctccg gaggtggtgg atccgatatc cagctgaccc agtctccagc ttctttggct 780
gtgtctctag ggcagagggc caccatctcc tgcaaggcca gccaaagtgt tgattatgat 840
ggtgatagtt atttgaactg gtaccaacag attccaggac agccacccaa actcctcatc 900
tatgatgcat ccaatctagt ttctgggatc ccacccagggt ttagtggcag tgggtctggg 960
acagacttca ccctcaacat ccctcctgtg gagaagggtg atgctgcaac ctatcactgt 1020
cagcaaagta ctgaggatcc gtggacgttc ggtggaggga ccaagctcga gatcaaagggt 1080
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tctggggctg agctggtgag gcctgggtcc tcagtgaaga tttcctgcaa ggcttctggc 1200
tatgcattca gtagctactg gatgaactgg gtgaagcaga ggcctggaca gggctctgag 1260
tggattggac agatttggcc tggagatggt gatactaact acaatggaaa gttcaagggt 1320
aaagccactc tgactgcaga cgaatcctcc agcacagcct acatgcaact cagcagccta 1380
gcatctgagg actctgcggt ctatttctgt gcaagacggg agactacgac ggtaggccgt 1440
tattactatg ctatggacta ctgggggcaa gggaccacgg tcaccgtctc ctcc 1494

<210> 363

<211> 498

<212> PRT

<213> artificial sequence

<220>

<223> VL2VH7xCD19 LHLH

<400> 363

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
100 105 110

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
115 120 125

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
145 150 155 160

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
165 170 175

Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
180 185 190

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
195 200 205

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr
210 215 220

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
225 230 235 240

Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro
245 250 255

Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys
260 265 270

Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr

275					280					285						
Gln	Gln	Ile	Pro	Gly	Gln	Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Asp	Ala	Ser	
290					295					300						
Asn	Leu	Val	Ser	Gly	Ile	Pro	Pro	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	
305					310					315					320	
Thr	Asp	Phe	Thr	Leu	Asn	Ile	His	Pro	Val	Glu	Lys	Val	Asp	Ala	Ala	
				325					330					335		
Thr	Tyr	His	Cys	Gln	Gln	Ser	Thr	Glu	Asp	Pro	Trp	Thr	Phe	Gly	Gly	
			340					345					350			
Gly	Thr	Lys	Leu	Glu	Ile	Lys	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	
		355					360					365				
Ser	Gly	Gly	Gly	Gly	Ser	Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Ala	Glu	
	370					375					380					
Leu	Val	Arg	Pro	Gly	Ser	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	
385						390					395				400	
Tyr	Ala	Phe	Ser	Ser	Tyr	Trp	Met	Asn	Trp	Val	Lys	Gln	Arg	Pro	Gly	
				405					410					415		
Gln	Gly	Leu	Glu	Trp	Ile	Gly	Gln	Ile	Trp	Pro	Gly	Asp	Gly	Asp	Thr	
			420					425					430			
Asn	Tyr	Asn	Gly	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Glu	
		435					440					445				
Ser	Ser	Ser	Thr	Ala	Tyr	Met	Gln	Leu	Ser	Ser	Leu	Ala	Ser	Glu	Asp	
		450				455					460					
Ser	Ala	Val	Tyr	Phe	Cys	Ala	Arg	Arg	Glu	Thr	Thr	Thr	Val	Gly	Arg	
465					470					475					480	
Tyr	Tyr	Tyr	Ala	Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	
				485					490					495		
Ser	Ser															

<210> 364
<211> 1497
<212> DNA
<213> artificial sequence

<220>
<223> VH7VL2xCD19 HLLH

<400> 364
gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaagggtg 60
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cctggacagg gtctggaatg gattggatac attaataccta gccgtgggta tactaattac 180
aatcagaagt tcaaggaccg cgtcacaatc actacagaca aatccaccag cacagcctac 240
atggaactga gcagcctgcg ttctgaggac actgcagtct attactgtgc aagatattat 300
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc 360
gaaggtaacta gtactgggtc tgggtggaagt ggagggttcag gtggagcaga cgacattgta 420
ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc 480
agagccagtc aaagtgtaag ttacatgaac tgggtaccagc agaagccggg caaggcaccc 540
aaaagatgga tttatgacac atccaaagtg gcttctggag tccttgctcg cttcagtggc 600
agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcgggtggcgg gaccaagggtg 720
gagatcaaata ccggagggtg tggatccgat atccagctga cccagtctcc agcttctttg 780
gctgtgtctc tagggcagag ggccaccatc tcctgcaagg ccagccaaag tggttgattat 840
gatggtgata gttatttgaa ctggtaccaa cagattccag gacagccacc caaactcctc 900
atctatgatg catccaatct agtttctggg atcccaccca ggtttagtgg cagtgggtct 960
gggacagact tcaccctcaa catccatcct gtggagaagg tggatgctgc aacctatcac 1020
tgtcagcaaa gtactgagga tccgtggacg ttcgggtggag ggaccaagct cgagatcaaa 1080
gggtggtggtg gttctggcgg cggcggctcc ggtggtggtg gttctcaggt gcagctgcag 1140
cagtctgggg ctgagctggt gaggcctggg tcctcagtga agatttcctg caaggcttct 1200
ggctatgcat tcagtagcta ctggatgaac tgggtgaagc agaggcctgg acagggtctt 1260
gagtggattg gacagatttg gcctggagat ggtgatacta actacaatgg aaagttcaag 1320
ggtaaagcca ctctgactgc agacgaatcc tccagcacag cctacatgca actcagcagc 1380
ctagcatctg aggactctgc ggtctatttc tgtgcaagac gggagactac gacggtaggc 1440
cgttattact atgctatgga ctactggggc caagggacca cggtcaccgt ctctcc 1497

<210> 365
<211> 499
<212> PRT
<213> artificial sequence

<220>
<223> VH7VL2xCD19 HLLH

<400> 365

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser
245 250 255

Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys
260 265 270

Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp
275 280 285

Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala
290 295 300

Ser Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser
305 310 315 320

Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val Asp Ala
325 330 335

Ala Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly
340 345 350

Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly
355 360 365

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Ala
370 375 380

Glu Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser
385 390 395 400

Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro
405 410 415

Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly Asp
420 425 430

Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp
435 440 445

Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu
450 455 460

Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val Gly
465 470 475 480

Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
485 490 495

Val Ser Ser

<210> 366
<211> 1494
<212> DNA
<213> artificial sequence

<220>
<223> VL3VH7xCD19 LHHL

<400> 366
gacattgtac tgaccagtc tccagcaact ctgtctctgt ctccagggga gcgtgccacc 60
ctgacctgca gagccagttc aagtgttaagt tacatgaact ggtaccagca gaagccgggc 120
aaggcaccca aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctcgc 180
ttcagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa 240
gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cggtggcggg 300
accaaggtgg agatcaaagg cgaaggtact agtactgggt ctggtggaag tggaggttca 360
ggtggagcag acgacgtcca actggtgcag tcaggggctg aagtgaaaaa acctggggcc 420
tcagtgaagg tgcctgcaa ggcttctggc tacaccttta ctaggtacac gatgcactgg 480
gtaaggcagg cacctggaca gggctctggaa tggattggat acattaatcc tagccgtgg 540
tatactaatt acaatcagaa gttcaaggac cgcgtcacia tcactacaga caaatccacc 600
agcacagcct acatggaact gagcagcctg cggttctgagg aactgcagt ctattactgt 660
gcaagatatt atgatgatca ttactgcctt gactactggg gccaaaggcac cacggtcacc 720
gtctcctccg gaggtgggtg atcccagggt cagctgcagc agtctggggc tgagctgggtg 780
aggcctgggt cctcagtga gatttcctgc aaggcttctg gctatgcatt cagtagctac 840
tgatgaact ggggtgaagca gaggcctgga cagggtcttg agtggattgg acagatttgg 900

cctggagatg gtgatactaa ctacaatgga aagttcaagg gtaaagccac tctgactgca 960
gacgaatcct ccagcacagc ctacatgcaa ctcagcagcc tagcatctga ggactctgcg 1020
gtctatttct gtgcaagacg ggagactacg acggtaggcc gttattacta tgctatggac 1080
tactggggcc aagggaccac ggtcaccgtc tctccggtg gtggtggttc tggcggcggc 1140
ggctccggtg gtggtggttc tgatatccag ctgacccagt ctccagcttc tttggctgtg 1200
tctctagggc agagggccac catctcctgc aaggccagcc aaagtgttga ttatgatggt 1260
gatagttatt tgaactggta ccaacagatt ccaggacagc cacccaaact cctcatctat 1320
gatgcatcca atctagtttc tgggatccca cccaggttta gtggcagtgg gtctgggaca 1380
gacttcaccc tcaacatcca tctgtggag aaggtggatg ctgcaaccta tcaactgtcag 1440
caaagtactg aggatccgtg gacgttcggt ggagggacca agctcgagat caaa 1494

<210> 367

<211> 498

<212> PRT

<213> artificial sequence

<220>

<223> VL3VH7xCD19 LHHL

<400> 367

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
100 105 110

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
 115 120 125

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
 130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
 145 150 155 160

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
 165 170 175

Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
 180 185 190

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
 195 200 205

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr
 210 215 220

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
 225 230 235 240

Val Ser Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly
 245 250 255

Ala Glu Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala
 260 265 270

Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg
 275 280 285

Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly
 290 295 300

Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala
 305 310 315 320

Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser
 325 330 335

Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val
 340 345 350

Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val
355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val
385 390 395 400

Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val
405 410 415

Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly
420 425 430

Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly
435 440 445

Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
450 455 460

Asn Ile His Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln
465 470 475 480

Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu
485 490 495

Ile Lys

<210> 368
<211> 1497
<212> DNA
<213> artificial sequence

<220>
<223> VH7VL3xCD19 HLHL

<400> 368
gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaaggtg 60
tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 120
cctggacagg gtctggaatg gattggatac attaatccta gccgtgggta tactaattac 180
aatcagaagt tcaaggaccg cgtcacaatc actacagaca aatccaccag cacagcctac 240

atggaactga gcagcctgcg ttctgaggac actgcagtct attactgtgc aagatattat 300
 gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctccctcaggc 360
 gaagg tacta gtactgggttc tgggtggaagt ggaggttcag gtggagcaga cgacattgta 420
 ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgacctgc 480
 agagccagtt caagtgt aag ttacatgaac tgggtaccagc agaagccggg caaggcaccc 540
 aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
 agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
 acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaagggtg 720
 gagatcaa at ccggagggtg tggatcccag gtgcagctgc agcagtctgg ggctgagctg 780
 gtgaggcctg ggtcctcagt gaagatttcc tgcaaggctt ctggctatgc attcagtagc 840
 tactggatga actgggtgaa gcagaggcct ggacagggtc ttgagtggat tggacagatt 900
 tggcctggag atggtgatac taactacaat ggaaagtcca agggtaaagc cactctgact 960
 gcagacgaat cctccagcac agcctacatg caactcagca gcctagcatc tgaggactct 1020
 gcggtctatt tctgtgcaag acgggagact acgacggtag gccgttatta ctatgctatg 1080
 gactactggg gccaaaggac cacggtcacc gtctcctccg gtggtggtgg ttctggcggc 1140
 ggcggctccg gtggtggtgg ttctgatatc cagctgacct agtctccagc ttctttggct 1200
 gtgtctctag ggcagagggc caccatctcc tgcaaggcca gccaaagtgt tgattatgat 1260
 ggtgatagtt atttgaactg gtaccaacag attccaggac agccacccaa actcctcatc 1320
 tatgatgcat ccaatctagt ttctgggatc ccacccaggt ttagtggcag tgggtctggg 1380
 acagacttca cctcaacat ccacctgtg gagaagggtg atgctgcaac ctatcactgt 1440
 cagcaaagta ctgaggatcc gtggacgttc ggtggaggga ccaagctcga gatcaaa 1497

<210> 369

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> VH7VL3xCD19 HLHL

<400> 369

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
 50 55 60

Lys Asp Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
 115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
 130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys
 145 150 155 160

Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser
 245 250 255

Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys

260

265

270

Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln
 275 280 285

Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp
 290 295 300

Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr
 305 310 315 320

Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala
 325 330 335

Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr
 340 345 350

Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr
 355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 370 375 380

Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala
 385 390 395 400

Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser
 405 410 415

Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro
 420 425 430

Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser
 435 440 445

Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 450 455 460

Leu Asn Ile His Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys
 465 470 475 480

Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu
 485 490 495

Glu Ile Lys

<210> 370
<211> 1494
<212> DNA
<213> artificial sequence

<220>
<223> VL3VH7xCD19 LHLH

<400> 370
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ctgacctgca gagccagttc aagtgttaagt tacatgaact ggtaccagca gaagccgggc 120
aaggcaccca aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctcgc 180
ttcagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa 240
gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cggtggcggg 300
accaaggtgg agatcaaagg cgaaggtact agtactgggt ctggtggaag tggaggttca 360
gggtggagcag acgacgtcca actggtgcag tcaggggctg aagtgaaaaa acctggggcc 420
tcagtgaagg tgtcctgcaa ggcttctggc tacaccttta ctaggtacac gatgcactgg 480
gtaaggcagg cacctggaca gggctctggaa tggattggat acattaatcc tagccgtggg 540
tatactaatt acaatcagaa gttcaaggac cgcgtcacia tcactacaga caaatccacc 600
agcacagcct acatggaact gagcagcctg cgcttctgagg aactgcagt ctattactgt 660
gcaagatatt atgatgatca ttactgcctt gactactggg gccaaaggcac cacggtcacc 720
gtctcctccg gaggtgggtg atccgatatc cagctgaccc agtctccagc ttctttggct 780
gtgtctctag ggcagagggc caccatctcc tgcaaggcca gccaaagtgt tgattatgat 840
ggatgatagt atttgaactg gtaccaacag attccaggac agccacccaa actcctcatc 900
tatgatgcat ccaatctagt ttctgggatc ccaccagggt ttagtggcag tgggtctggg 960
acagacttca ccctcaacat ccctcctgtg gagaaggtgg atgctgcaac ctatcactgt 1020
cagcaaagta ctgaggatcc gtggacgttc ggtggaggga ccaagctcga gatcaaaggt 1080
gggtgggtgg ctggcggcgg cggctccggg ggtgggtgggt ctccaggtgca gctgcagcag 1140
tctgggggct agctgggtgag gcctgggtcc tcagtgaaga ttctctgcaa ggcttctggc 1200
tatgcattca gtagctactg gatgaactgg gtgaagcaga ggcctggaca ggggtcttgag 1260
tggattggac agatttggcc tggagatggg gatactaact acaatggaaa gttcaagggt 1320
aaagccactc tgactgcaga cgaatcctcc agcacagcct acatgcaact cagcagccta 1380

gcattctgagg actctgcggt ctatttctgt gcaagacggg agactacgac ggtagggcgt 1440
tattactatg ctatggacta ctggggccaa gggaccacgg tcaccgtctc ctcc 1494

<210> 371
<211> 498
<212> PRT
<213> artificial sequence

<220>
<223> VL3VH7xCD19 LHLH

<400> 371

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
100 105 110

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
115 120 125

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
145 150 155 160

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
165 170 175

Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
180 185 190

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
195 200 205

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr
210 215 220

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
225 230 235 240

Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro
245 250 255

Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys
260 265 270

Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr
275 280 285

Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser
290 295 300

Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly
305 310 315 320

Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val Asp Ala Ala
325 330 335

Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly
340 345 350

Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly
355 360 365

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu
370 375 380

Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly
385 390 395 400

Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly
405 410 415

Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr
 420 425 430

Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu
 435 440 445

Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu Asp
 450 455 460

Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val Gly Arg
 465 470 475 480

Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
 485 490 495

Ser Ser

<210> 372
 <211> 1497
 <212> DNA
 <213> artificial sequence

<220>
 <223> VH7VL3xCD19 HLLH

<400> 372
 gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaagggtg 60
 tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 120
 cctggacagg gtctggaatg gattggatac attaataccta gccgtgggtta tactaattac 180
 aatcagaagt tcaaggaccg cgtcacaatc actacagaca aatccaccag cacagcctac 240
 atggaactga gcagcctgcg ttctgaggac actgcagtct attactgtgc aagatattat 300
 gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc 360
 gaaggtaacta gtactgggttc tgggtggaagt ggagggttcag gtggagcaga cgacattgta 420
 ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgacctgc 480
 agagccagtt caagtgtaag ttacatgaac tgggtaccagc agaagccggg caaggcaccc 540
 aaaagatgga tttatgacac atccaaagtg gcttctggag tccttgctcg cttcagtggc 600
 agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
 acttattact gccaacagtg gagtagtaac ccgctcacgt tcgggtggcgg gaccaagggtg 720
 gagatcaaatt ccggagggtgg tggatccgat atccagctga cccagtctcc agcttctttg 780

gctgtgtctc tagggcagag ggccaccatc tcctgcaagg ccagccaaag tgttgattat 840
 gatggtgata gttatttgaa ctggtaccaa cagattccag gacagccacc caaactcctc 900
 atctatgatg catccaatct agtttctggg atcccaccca ggtttagtgg cagtgggtct 960
 gggacagact tcaccctcaa catccatcct gtggagaagg tggatgctgc aacctatcac 1020
 tgtcagcaaa gtactgagga tccgtggacg ttcggtggag ggaccaagct cgagatcaaa 1080
 ggtggtggtg gttctggcgg cggcggctcc ggtggtggtg gttctcaggt gcagctgcag 1140
 cagtctgggg ctgagctggt gaggcctggg tcctcagtga agatttcctg caaggcttct 1200
 ggctatgcat tcagtagcta ctggatgaac tgggtgaagc agaggcctgg acagggctct 1260
 gagtggattg gacagatttg gcctggagat ggtgatacta actacaatgg aaagttcaag 1320
 ggtaaagcca ctctgactgc agacgaatcc tccagcacag cctacatgca actcagcagc 1380
 ctagcatctg aggactctgc ggtctatttc tgtgcaagac gggagactac gacggtaggc 1440
 cgttattact atgctatgga ctactggggc caagggacca cggtcaccgt ctctctcc 1497

<210> 373

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> VH7VL3xCD19 HLLH

<400> 373

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
 50 55 60

Lys Asp Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys
145 150 155 160

Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser
245 250 255

Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys
260 265 270

Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp
275 280 285

Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala
290 295 300

Ser Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser
305 310 315 320

Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val Asp Ala
325 330 335

Ala Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly
 340 345 350

Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly
 355 360 365

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Ala
 370 375 380

Glu Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser
 385 390 395 400

Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro
 405 410 415

Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly Asp
 420 425 430

Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp
 435 440 445

Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu
 450 455 460

Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val Gly
 465 470 475 480

Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
 485 490 495

Val Ser Ser

<210> 374
 <211> 1497
 <212> DNA
 <213> artificial sequence

<220>
 <223> CD19xVH5/VL1 HLHL

<400> 374
 caggtgcagc tgcagcagtc tggggctgag ctggtgaggc ctgggtcctc agtgaagatt 60
 tcctgcaagg cttctggcta tgcattcagt agctactgga tgaactgggt gaagcagagg 120

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cctggacagg gtcttgagtg gattggacag atttggcctg gagatgggtga tactaactac 180
aatggaaagt tcaagggtaa agccactctg actgcagacg aatcctccag cacagcctac 240
atgcaactca gcagcctagc atctgaggac tctgcggtct atttctgtgc aagacgggag 300
actacgacgg taggccgtta ttactatgct atggactact ggggccaagg gaccacggtc 360
accgtctcct ccggtggtgg tggttctggc ggcggcggct ccggtggtgg tggttctgat 420
atccagctga ccagctctcc agcttctttg gctgtgtctc tagggcagag ggccaccatc 480
tcttgcaagg ccagccaaag tgttgattat gatggtgata gttatattgaa ctggtaccaa 540
cagattccag gacagccacc caaactcctc atctatgatg catccaatct agtttctggg 600
atcccaccca ggtttagtgg cagtgggtct gggacagact tcaccctcaa catccatcct 660
gtggagaagg tggatgctgc aacctatcac tgtcagcaaa gtactgagga tccgtggacg 720
ttcgggtggag ggaccaagct cgagatcaaa tccggaggtg gtggatccga cgtccaactg 780
gtgcagtcag gggctgaagt gaaaaaacct ggggcctcag tgaagggtgc ctgcaaggct 840
tctggctaca cctttactag gtacacgatg cactgggtaa ggcaggcacc tggacagggt 900
ctggaatgga ttggatacat taatcctagc cgtgggttata ctaattacgc agacagcgtc 960
aagggccgct tcacaatcac tacagacaaa tccaccagca cagcctacat ggaactgagc 1020
agcctgcgtt ctgaggacac tgcaacctat tactgtgcaa gatattatga tgatcattac 1080
tgccttgact actggggcca aggcaccacg gtcaccgtct cctcaggcga aggtactagt 1140
actggttctg gtggaagtgg aggttcaggt ggagcagacg acattcagat gacccagtct 1200
ccatctagcc tgtctgcac tgtcggggac cgtgtcacca tcacctgcag agccagtcaa 1260
agtgtaagtt acatgaactg gtaccagcag aagccgggca aggcacccaa aagatggatt 1320
tatgacacat ccaaagtggc ttctggagtc cctgctcgct tcagtggcag tgggtctggg 1380
accgactact ctctcacaat caacagcttg gaggtgaag atgctgccac ttattactgc 1440
caacagtgga gtagtaacct gctcacgttc ggtggcggga ccaaggtgga gatcaaa 1497

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<210> 375

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> CD19xVH5VL1 HLHL

<400> 375

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr
20 25 30

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr
130 135 140

Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile
145 150 155 160

Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu
165 170 175

Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
180 185 190

Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser
195 200 205

Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val
210 215 220

Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr
225 230 235 240

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser

245

250

255

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
260 265 270

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
275 280 285

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
290 295 300

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
305 310 315 320

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
325 330 335

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
340 345 350

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
355 360 365

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
370 375 380

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser
385 390 395 400

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
405 410 415

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
420 425 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
435 440 445

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
450 455 460

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
465 470 475 480

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
485 490 495

Glu Ile Lys

<210> 376
<211> 1494
<212> DNA
<213> artificial sequence

<220>
<223> CD19xVL1VH5 LHLH

<400> 376
gatatccagc tgaccagtc tccagcttct ttggctgtgt ctctagggca gagggccacc 60
atctcctgca aggccagcca aagtgttgat tatgatggtg atagttatTT gaactggtac 120
caacagattc caggacagcc acccaaactc ctcatctatg atgcatccaa tctagtTTtct 180
gggatcccac ccaggTTtag tggcagtggg tctgggacag acttcaccct caacatccat 240
cctgtggaga aggtggatgc tgcaacctat cactgtcagc aaagtactga ggatccgtgg 300
acgttcggtg gagggaccaa gctcgagatc aaaggtggtg gtggttctgg cggcggcggc 360
tccggtggtg gtggttctca ggtgcagctg cagcagtctg gggctgagct ggtgaggcct 420
gggtcctcag tgaagatttc ctgcaaggct tctggctatg cattcagtag ctactggatg 480
aactgggtga agcagaggcc tggacagggt cttgagtgga ttggacagat ttggcctgga 540
gatggtgata ctaactacaa tggaaagttc aagggtaaag ccactctgac tgcagacgaa 600
tcctccagca cagcctacat gcaactcagc agcctagcat ctgaggactc tgcggtctat 660
ttctgtgcaa gacgggagac tacgacggta ggccgttatt actatgctat ggactactgg 720
ggccaagggg ccacggtcac cgtctcctcc ggaggtggtg gatccgacat tcagatgacc 780
cagtctccat ctagcctgtc tgcattctgtc ggggaccgtg tcaccatcac ctgcagagcc 840
agtcaaagtg taagtTacat gaactggtac cagcagaagc cgggcaaggc acccaaaaga 900
tggatttatg acacatccaa agtggcttct ggagtcctctg ctcgcttcag tggcagtggg 960
tctgggaccg actactctct cacaatcaac agcttggagg ctgaagatgc tgccacttat 1020
tactgccaac agtggagtag taacccgctc acgttcggtg gcgggaccaa ggtggagatc 1080
aaaggcgaag gtactagtag tggttctggt ggaagtggag gttcaggtgg agcagacgac 1140
gtccaactgg tgcagtcagg ggctgaagtg aaaaaacctg gggcctcagt gaaggtgtcc 1200
tgcaaggctt ctggctacac ctttactagg tacacgatgc actgggtaag gcaggcacct 1260

ggacaggggtc tggaatggat tggatacatt aatcctagcc gtgggttatac taattacgca 1320
gacagcgtca agggccgctt cacaatcact acagacaaat ccaccagcac agcctacatg 1380
gaactgagca gcctgcgttc tgaggacact gcaacctatt actgtgcaag atattatgat. 1440
gatcattact gccttgacta ctgggggcaa ggcaccacgg tcaccgtctc ctca 1494

<210> 377
<211> 498
<212> PRT
<213> artificial sequence

<220>
<223> CD19xVL1VH5 LHLH

<400> 377

Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
20 25 30

Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65 70 75 80

Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
85 90 95

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
115 120 125

Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val
130 135 140

Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met
145 150 155 160

Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln
165 170 175

Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly
180 185 190

Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln
195 200 205

Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg
210 215 220

Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp
225 230 235 240

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp
245 250 255

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
260 265 270

Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Tyr Met Asn
275 280 285

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp
290 295 300

Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly
305 310 315 320

Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp
325 330 335

Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe
340 345 350

Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr Gly
355 360 365

Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu Val
370 375 380

Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser
385 390 395 400

Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val
405 410 415

Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro
420 425 430

Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr
435 440 445

Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser
450 455 460

Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr Asp
465 470 475 480

Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
485 490 495

Ser Ser

<210> 378
<211> 1497
<212> DNA
<213> artificial sequence

<220>
<223> CD19xVL1VH5 HLLH

<400> 378
caggtgcagc tgcagcagtc tggggctgag ctggtgaggc ctgggtcctc agtgaagatt 60
tcctgcaagg cttctggcta tgcattcagt agctactgga tgaactgggt gaagcagagg 120
cctggacagg gtcttgagtg gattggacag atttggcctg gagatgggtga tactaactac 180
aatggaaagt tcaagggtaa agccactctg actgcagacg aatcctccag cacagcctac 240
atgcaactca gcagcctagc atctgaggac tctgcggtct atttctgtgc aagacgggag 300
actacgacgg taggccgtta ttactatgct atggactact ggggcccaagg gaccacggtc 360
accgtctcct ccggtggtgg tggttctggc ggcggcggct ccggtggtgg tggttctgat 420
atccagctga ccagctctcc agcttctttg gctgtgtctc tagggcagag ggccaccatc 480
tcctgcaagg ccagccaaag tggtgattat gatggtgata gttatttgaa ctggtaccaa 540
cagattccag gacagccacc caaactcctc atctatgatg catccaatct agtttctggg 600
atcccacca ggtttagtgg cagtgggtct gggacagact tcaccctcaa catccatcct 660

gtggagaagg tggatgctgc aacctatcac tgtcagcaaa gtactgagga tccgtggacg 720
 ttcggtggag ggaccaagct cgagatcaaa tccggagggtg gtggatccga cattcagatg 780
 acccagtctc catctagcct gtctgcatct gtcggggacc gtgtcaccat cacctgcaga 840
 gccagtcaaa gtgtaagtta catgaactgg taccagcaga agccgggcaa ggcacccaaa 900
 agatggattt atgacacatc caaagtgggt tctggagtcc ctgctcgctt cagtggcagt 960
 gggctctggga ccgactactc tctcacaatc aacagcttgg aggctgaaga tgctgccact 1020
 tattactgcc aacagtggag tagtaacccg ctcacgttcg gtggcgggac caaggtggag 1080
 atcaaaggcg aaggtactag tactggttct ggtggaagtg gaggttcagg tggagcagac 1140
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 tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 1260
 cctggacagg gtctggaatg gattggatac attaatccta gccgtgggtta tactaattac 1320
 gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 1380
 atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 1440
 gatgatcatt actgccttga ctactggggc caaggcacca cggtcacctg ctctctca 1497

<210> 379
 <211> 499
 <212> PRT
 <213> artificial sequence

<220>
 <223> CD19xVL1VH5 HLLH

<400> 379

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser
 1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr
 20 25 30

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe
 50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr
 65 70 75 80

Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr
130 135 140

Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile
145 150 155 160

Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu
165 170 175

Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
180 185 190

Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser
195 200 205

Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val
210 215 220

Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr
225 230 235 240

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
260 265 270

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
275 280 285

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
290 295 300

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
305 310 315 320

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
325 330 335

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
340 345 350

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
355 360 365

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
370 375 380

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
385 390 395 400

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
405 410 415

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
420 425 430

Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe
435 440 445

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
450 455 460

Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr
465 470 475 480

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
485 490 495

Val Ser Ser

<210> 380
<211> 1497
<212> DNA
<213> artificial sequence

<220>
<223> CD19xVH5VL2 HLHL

<400> 380

caggtgcagc tgcagcagtc tggggctgag ctggtgaggc ctgggtcctc agtgaagatt 60
tcctgcaagg cttctggcta tgcattcagt agctactgga tgaactgggt gaagcagagg 120
cctggacagg gtcttgagtg gattggacag atttggcctg gagatgggtga tactaactac 180
aatggaaagt tcaagggtaa agccactctg actgcagacg aatcctccag cacagcctac 240
atgcaactca gcagcctagc atctgaggac tctgcggtct atttctgtgc aagacgggag 300
actacgacgg taggccgtta ttactatgct atggactact ggggccaaagg gaccacggtc 360
accgtctcct ccggtgggtg tggttctggc ggcggcggtc ccggtgggtg tggttctgat 420
atccagctga ccagctctcc agcttctttg gctgtgtctc tagggcagag ggccaccatc 480
tcctgcaagg ccagccaaag tggtgattat gatgggtgata gttatttgaa ctgggtaccaa 540
cagattccag gacagccacc caaactcctc atctatgatg catccaatct agtttctggg 600
atcccaccca ggtttagtgg cagtgggtct gggacagact tcaccctcaa catccatcct 660
gtggagaagg tggatgctgc aacctatcac tgtcagcaaa gtactgagga tccgtggacg 720
ttcgggtggag ggaccaagct cgagatcaaa tccggagggtg gtggatccga cgtccaactg 780
gtgcagtcag gggctgaagt gaaaaaacct ggggcctcag tgaaggtgtc ctgcaaggct 840
tctggctaca cctttactag gtacacgatg cactgggtaa ggcaggcacc tggacagggt 900
ctggaatgga ttggatacat taatcctagc cgtgggttata ctaattacgc agacagcgtc 960
aagggccgct tcacaatcac tacagacaaa tccaccagca cagcctacat ggaactgagc 1020
agcctgcgtt ctgaggacac tgcaacctat tactgtgcaa gatattatga tgatcattac 1080
tgccttgact actggggcca aggcaccacg gtcaccgtct cctcaggcga aggtactagt 1140
actggttctg gtggaagtgg aggttcaggt ggagcagacg acattgtact gaccagctct 1200
ccagcaactc tgtctctgtc tccaggggag cgtgccaccc tgagctgcag agccagtcaa 1260
agtgtaagtt acatgaactg gtaccagcag aagccgggca aggcacccaa aagatggatt 1320
tatgacacat ccaaagtggc ttctggagtc cctgctcgtc tcagtggcag tgggtctggg 1380
accgactact ctctcacaat caacagcttg gaggtgaag atgctgccac ttattactgc 1440
caacagtgga gtagtaaccc gctcacgttc ggtggcggga ccaaggtgga gatcaaa 1497

<210> 381
<211> 499
<212> PRT
<213> artificial sequence

<220>
<223> CD19xVH5VL2 HLHL

<400> 381

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr
20 25 30

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr
130 135 140

Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile
145 150 155 160

Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu
165 170 175

Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
180 185 190

Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser
195 200 205

Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val
210 215 220

Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr

225		230		235		240
Phe Gly Gly Gly Thr	Lys Leu Glu Ile	Lys Ser Gly Gly Gly Gly Ser				
	245	250			255	
Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala						
	260	265			270	
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr						
	275	280			285	
Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile						
	290	295			300	
Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val						
	305	310			315	320
Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr						
	325	330			335	
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys						
	340	345			350	
Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly						
	355	360			365	
Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly						
	370	375			380	
Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser						
	385	390			395	400
Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys						
	405	410			415	
Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro						
	420	425			430	
Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser						
	435	440			445	
Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser						
	450	455			460	

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
465 470 475 480

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
485 490 495

Glu Ile Lys

<210> 382
<211> 1494
<212> DNA
<213> artificial sequence

<220>
<223> CD19xVL2VH5 LHLH

<400> 382
gatatccagc tgacccagtc tccagcttct ttggctgtgt ctctagggca gagggccacc 60
atctcctgca aggccagcca aagtgttgat tatgatgggtg atagttattt gaactggtac 120
caacagattc caggacagcc acccaaactc ctcatctatg atgcatccaa tctagtttct 180
gggatcccac ccaggttttag tggcagtggg tctgggacag acttcaccct caacatccat 240
cctgtggaga aggtggatgc tgcaacctat cactgtcagc aaagtactga ggatccgtgg 300
acgttcgggtg gagggaccaa gctcgagatc aaaggtgggtg gtggttcttg cggcggcggc 360
tccggtgggtg gtggttctca ggtgcagctg cagcagtctg gggctgagct ggtgaggcct 420
gggtcctcag tgaagatttc ctgcaaggct tctggctatg cattcagtag ctactggatg 480
aactgggtga agcagaggcc tggacagggt cttgagtgga ttggacagat ttggcctgga 540
gatggtgata ctaactacaa tggaaagttc aagggtaaag ccactctgac tgcagacgaa 600
tcctccagca cagcctacat gcaactcagc agcctagcat ctgaggactc tgcggtctat 660
ttctgtgcaa gacgggagac tacgacggta ggccgttatt actatgctat ggactactgg 720
ggccaaggga ccacggtcac cgtctcctcc ggaggtgggtg gatccgacat tgtactgacc 780
cagtctccag caactctgtc tctgtctcca ggggagcgtg ccaccctgag ctgcagagcc 840
agtcaaagtg taagttacat gaactggtac cagcagaagc cgggcaaggc acccaaaaga 900
tggatttatg acacatccaa agtggcttct ggagtcctctg ctcgcttcag tggcagtggg 960
tctgggaccg actactctct cacaatcaac agcttggagg ctgaagatgc tgccacttat 1020
tactgccaac agtggagtag taaccgctc acgttcgggtg gcgggaccaa ggtggagatc 1080
aaaggcgaag gtactagtag tggttctggg ggaagtggag gttcaggtgg agcagacgac 1140

```

gtccaactgg tgcagtcagg ggctgaagtg aaaaaacctg gggcctcagt gaagggtgcc 1200
tgcaaggctt ctggctacac ctttactagg tacacgatgc actgggtaag gcaggcacct 1260
ggacagggtc tggaatggat tggatacatt aatcctagcc gtgggttatac taattacgca 1320
gacagcgtca agggccgctt cacaatcact acagacaaat ccaccagcac agcctacatg 1380
gaactgagca gcctgcgttc tgaggacact gcaacctatt actgtgcaag atattatgat 1440
gatcattact gccttgacta ctgggggcaa ggcaccacgg tcaccgtctc ctca 1494

```

<210> 383

<211> 498

<212> PRT

<213> artificial sequence

<220>

<223> CD19xVL2VH5 LHLH

<400> 383

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Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1           5           10           15

```

```

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
          20           25           30

```

```

Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
35           40           45

```

```

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
50           55           60

```

```

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65           70           75           80

```

```

Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
          85           90           95

```

```

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
100           105           110

```

```

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
115           120           125

```

```

Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val
130           135           140

```


Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met
145 150 155 160

Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln
165 170 175

Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly
180 185 190

Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln
195 200 205

Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg
210 215 220

Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp
225 230 235 240

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp
245 250 255

Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu
260 265 270

Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met Asn
275 280 285

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp
290 295 300

Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly
305 310 315 320

Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp
325 330 335

Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe
340 345 350

Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr Gly
355 360 365

Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu Val
370 375 380

Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser
385 390 395 400

Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val
405 410 415

Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro
420 425 430

Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr
435 440 445

Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser
450 455 460

Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr Asp
465 470 475 480

Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
485 490 495

Ser Ser

<210> 384
<211> 1497
<212> DNA
<213> artificial sequence

<220>
<223> CD19xVL2VH5 HLLH

<400> 384
caggtgcagc tgcagcagtc tggggctgag ctggtgaggc ctgggtcctc agtgaagatt 60
tcctgcaagg cttctggcta tgcattcagt agctactgga tgaactgggt gaagcagagg 120
cctggacagg gtcttgagtg gattggacag atttggcctg gagatgggtga tactaactac 180
aatggaaagt tcaagggtaa agccactctg actgcagacg aatcctccag cacagcctac 240
atgcaactca gcagcctagc atctgaggac tctgcggtct atttctgtgc aagacgggag 300
actacgacgg taggccgtta ttactatgct atggactact ggggccaagg gaccacggtc 360
accgtctcct ccggtgggtgg tggttctggc ggcggcggct ccggtgggtg tggttctgat 420
atccagctga ccagctctcc agcttctttg gctgtgtctc tagggcagag ggccaccatc 480
tcctgcaagg ccagccaaag tgttgattat gatggtgata gttatttgaa ctggtaccaa 540

cagattccag gacagccacc caaactcctc atctatgatg catccaatct agtttctggg 600
 atccccacca ggttttagtgg cagtgggtct gggacagact tcaccctcaa catccatcct 660
 gtggagaagg tggatgctgc aacctatcac tgtcagcaaa gtactgagga tccgtggacg 720
 ttcggtggag ggaccaagct cgagatcaaa tccggagggtg gtggatccga cattgtactg 780
 acccagtctc cagcaactct gtctctgtct ccaggggagc gtgccaccct gagctgcaga 840
 gccagtcaaa gtgtaagtta catgaactgg taccagcaga agccgggcaa ggcacccaaa 900
 agatggattt atgacacatc caaagtggct tctggagtcc ctgctcgctt cagtggcagt 960
 gggctctggga ccgactactc tctcacaatc aacagcttgg aggctgaaga tgctgccact 1020
 tattactgcc aacagtggag tagtaaccgg ctacggttcg gtggcgggac caaggtggag 1080
 atcaaaggcg aaggtactag tactggttct ggtggaagtg gaggttcagg tggagcagac 1140
 gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaagggtg 1200
 tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 1260
 cctggacagg gtctggaatg gattggatac attaatacta gccgtgggta tactaattac 1320
 gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 1380
 atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 1440
 gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctcctca 1497

<210> 385
 <211> 499
 <212> PRT
 <213> artificial sequence

<220>
 <223> CD19xVL2VH5 HLLH

<400> 385

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser
 1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr
 20 25 30

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe
 50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr
130 135 140

Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile
145 150 155 160

Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu
165 170 175

Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
180 185 190

Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser
195 200 205

Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val
210 215 220

Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr
225 230 235 240

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
260 265 270

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
275 280 285

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
290 295 300

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
305 310 315 320

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
325 330 335

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
340 345 350

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
355 360 365

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
370 375 380

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
385 390 395 400

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
405 410 415

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
420 425 430

Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe
435 440 445

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
450 455 460

Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr
465 470 475 480

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
485 490 495

Val Ser Ser

<210> 386

<211> 1497

<212> DNA

<213> artificial sequence

<220>

<223> CD19xVH5VL3 HLHL

<400> 386

caggtgcagc tgcagcagtc tggggctgag ctggtgaggc ctgggtcctc agtgaagatt	60
tcctgcaagg cttctggcta tgcattcagt agctactgga tgaactgggt gaagcagagg	120
cctggacagg gtcttgagtg gattggacag atttggcctg gagatgggtga tactaactac	180
aatggaaagt tcaagggtaa agccactctg actgcagacg aatcctccag cacagcctac	240
atgcaactca gcagcctagc atctgaggac tctgcggtct atttctgtgc aagacgggag	300
actacgacgg taggccgtta ttactatgct atggactact ggggcccaagg gaccacggtc	360
accgtctcct ccggtggtgg tggttctggc ggcggcggtt ccggtggtgg tggttctgat	420
atccagctga ccagctctcc agcttctttg gctgtgtctc tagggcagag ggccaccatc	480
tcctgcaagg ccagccaaag tggtgattat gatggtgata gttatttgaa ctggtaccaa	540
cagattccag gacagccacc caaactcctc atctatgatg catccaatct agtttctggg	600
atcccaccca ggtttagtgg cagtgggtct gggacagact tcaccctcaa catccatcct	660
gtggagaagg tggatgctgc aacctatcac tgtcagcaaa gtactgagga tccgtggacg	720
ttcgggtggag ggaccaagct cgagatcaaa tccggaggtg gtggatccga cgtccaactg	780
gtgcagtcag gggctgaagt gaaaaaacct ggggcctcag tgaagggtgc ctgcaaggct	840
tctggctaca cctttactag gtacacgatg cactgggtaa ggcaggcacc tggacagggt	900
ctggaatgga ttggatacat taatcctagc cgtgggttata ctaattacgc agacagcgtc	960
aagggccgct tcacaatcac tacagacaaa tccaccagca cagcctacat ggaactgagc	1020
agcctgcgtt ctgaggacac tgcaacctat tactgtgcaa gatattatga tgatcattac	1080
tgccttgact actggggcca aggcaccacg gtcaccgtct cctcaggcga aggtactagt	1140
actggttctg gtggaagtgg aggttcaggt ggagcagacg acattgtact gaccagtcct	1200
ccagcaactc tgtctctgtc tccaggggag cgtgccaccc tgacctgcag agccagttca	1260
agtgtaagtt acatgaactg gtaccagcag aagccgggca aggcacccaa aagatggatt	1320
tatgacacat ccaaagtggc ttctggagtc cctgctcgct tcagtggcag tgggtctggg	1380
accgactact ctctcacaat caacagcttg gaggtgaag atgctgccac ttattactgc	1440
caacagtgga gtagtaaccc gctcacgttc ggtggcgagg ccaaggtgga gatcaaa	1497

<210> 387

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> CD19xVH5VL3 HLHL

<400> 387

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr
20 25 30

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr
130 135 140

Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile
145 150 155 160

Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu
165 170 175

Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
180 185 190

Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser
195 200 205

Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val

210		215		220
Asp 225	Ala	Ala	Thr	Tyr
		His 230	Cys	Gln
			Gln	Ser
				Thr 235
			Glu	Asp
			Pro	Trp
				Thr 240
Phé	Gly	Gly	Gly	Thr
				Lys 245
			Leu	Glu
			Ile	Lys 250
				Ser
			Gly	Gly
			Gly	Gly
				Ser 255
Asp	Val	Gln	Leu	Val
				Gln 260
			Ser	Gly
				Ala 265
			Glu	Val
			Lys	Lys
				Pro 270
			Gly	Ala
Ser	Val	Lys	Val	Ser
				Cys 275
			Lys	Ala
				Ser 280
			Gly	Tyr
			Thr	Thr
				Phe 285
				Thr
				Arg
				Tyr
Thr	Met	His	Trp	Val
				Arg 290
			Gln	Ala
				Pro 295
			Gly	Gln
				Gly 300
			Leu	Glu
			Trp	Ile
Gly	Tyr	Ile	Asn	Pro
				Ser 305
			Arg	Gly
				Tyr 310
			Thr	Asn
				Tyr 315
			Ala	Asp
			Ser	Val
				Ser 320
Lys	Gly	Arg	Phe	Thr
				Ile 325
			Thr	Thr
				Asp 330
			Lys	Ser
				Thr 335
			Ser	Thr
				Ala
				Tyr 335
Met	Glu	Leu	Ser	Ser
				Leu 340
			Arg	Ser
				Glu 345
			Asp	Thr
				Ala 350
			Thr	Tyr
				Tyr 355
			Cys	Leu
				Asp 360
			Tyr	Trp
				Gly 365
			Gln	Gly
Thr	Thr	Val	Thr	Val
				Ser 370
			Ser	Ser
				Gly 375
			Glu	Gly
				Thr 380
			Ser	Thr
				Gly
			Ser	Gly
Gly	Ser	Gly	Gly	Ser
				Gly 385
			Ala	Asp
				Asp 390
			Ile	Val
				Leu 395
			Thr	Gln
				Ser 400
Pro	Ala	Thr	Leu	Ser
				Leu 405
			Ser	Pro
				Gly 410
			Glu	Arg
				Ala 415
			Thr	Leu
				Thr 415
			Cys	
Arg	Ala	Ser	Ser	Val
				Ser 420
			Tyr	Met
				Asn 425
			Trp	Tyr
				Gln 430
			Gln	Lys
				Pro
Gly	Lys	Ala	Pro	Lys
				Arg 435
			Trp	Ile
				Tyr 440
			Asp	Thr
				Ser 445
			Lys	Val
				Ala
				Ser

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
450 455 460

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
465 470 475 480

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
485 490 495

Glu Ile Lys

<210> 388

<211> 1494

<212> DNA

<213> artificial sequence

<220>

<223> CD19xVL3VH5 LHLH

<400> 388

gatatccagc tgacccagtc tccagcttct ttggctgtgt ctctagggca gagggccacc	60
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caacagattc caggacagcc acccaaactc ctcatctatg atgcatccaa tctagtttct	180
gggatcccac ccaggttttag tggcagtggtg tctgggacag acttcaccct caacatccat	240
cctgtggaga aggtggatgc tgcaacctat cactgtcagc aaagtactga ggatccgtgg	300
acgttcggtg gagggaccaa gctcgagatc aaaggtggtg gtggttctgg cggcggcggc	360
tccggtggtg gtggttctca ggtgcagctg cagcagtctg gggctgagct ggtgaggcct	420
gggtcctcag tgaagatttc ctgcaaggct tctggctatg cattcagtag ctactggatg	480
aactgggtga agcagaggcc tggacagggt cttgagtgga ttggacagat ttggcctgga	540
gatggtgata ctaactacaa tggaaagttc aagggtaaag ccactctgac tgcagacgaa	600
tcctccagca cagcctacat gcaactcagc agcctagcat ctgaggactc tgcggtctat	660
ttctgtgcaa gacgggagac tacgacggta ggccgttatt actatgctat ggactactgg	720
ggccaaggga ccacggtcac cgtctcctcc ggaggtggtg gatccgacat tgtactgacc	780
cagtctccag caactctgtc tctgtctcca ggggagcgtg ccaccctgac ctgcagagcc	840
agttcaagtg taagttacat gaactggtac cagcagaagc cgggcaaggc acccaaaaga	900
tggatttatg acacatccaa agtggcttct ggagtcctctg ctgccttcag tggcagtggtg	960
tctgggaccg actactctct cacaatcaac agcttggagg ctgaagatgc tgccacttat	1020

tactgccaac agtggagtag taacccgctc acgttcggtg gcgggaccaa ggtggagatc 1080
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gtccaactgg tgcagtcagg ggctgaagtg aaaaaacctg gggcttcagt gaaggtgtcc 1200
tgcaaggctt ctggctacac ctttactagg tacacgatgc actgggtaag gcaggcacct 1260
ggacaggggtc tggaatggat tggatacatt aatcctagcc gtgggttatac taattacgca 1320
gacagcgtca agggccgctt cacaatcact acagacaaat ccaccagcac agcctacatg 1380
gaactgagca gcctgcgttc tgaggacact gcaacctatt actgtgcaag atattatgat 1440
gatcattact gccttgacta ctggggccaa ggcaccacgg tcaccgtctc ctca 1494

<210> 389

<211> 498

<212> PRT

<213> artificial sequence

<220>

<223> CD19xVL3VH5 LHLH

<400> 389

Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
20 25 30

Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65 70 75 80

Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
85 90 95

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
115 120 125

Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val
130 135 140

Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met
145 150 155 160

Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln
165 170 175

Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly
180 185 190

Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln
195 200 205

Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg
210 215 220

Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp
225 230 235 240

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp
245 250 255

Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu
260 265 270

Arg Ala Thr Leu Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met Asn
275 280 285

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp
290 295 300

Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly
305 310 315 320

Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp
325 330 335

Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe
340 345 350

Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr Gly
355 360 365

Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu Val
370 375 380

Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser
385 390 395 400

Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val
405 410 415

Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro
420 425 430

Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr
435 440 445

Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser
450 455 460

Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr Asp
465 470 475 480

Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
485 490 495

Ser Ser

<210> 390
<211> 1497
<212> DNA
<213> artificial sequence

<220>
<223> CD19xVL3VH5 HLLH

<400> 390
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cctggacagg gtcttgagtg gattggacag atttggcctg gagatgggtga tactaactac 180
aatggaaagt tcaagggtaa agccactctg actgcagacg aatcctccag cacagcctac 240
atgcaactca gcagcctagc atctgaggac tctgcggtct atttctgtgc aagacgggag 300
actacgacgg taggccgtta ttactatgct atggactact ggggcccaagg gaccacggtc 360
accgtctcct ccggtggtgg tggttctggc ggcggcggct ccggtggtgg tggttctgat 420

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atccagctga cccagtctcc agcttctttg gctgtgtctc tagggcagag ggccaccatc 480
tcctgcaagg ccagccaaag tgttgattat gatggtgata gttatttgaa ctggtaccaa 540
cagattccag gacagccacc caaactcctc atctatgatg catccaatct agtttctggg 600
atcccaccca ggtttagtgg cagtgggtct gggacagact tcaccctcaa catccatcct 660
gtggagaagg tggatgctgc aacctatcac tgtcagcaaa gtactgagga tccgtggacg 720
ttcgggtggag ggaccaagct cgagatcaaa tccggaggtg gtggatccga cattgtactg 780
accagtcctc cagcaactct gtctctgtct ccaggggagc gtgccaccct gacctgcaga 840
gccagttcaa gtgtaagtta catgaactgg taccagcaga agccgggcaa ggcacccaaa 900
agatggattt atgacacatc caaagtggct tctggagtcc ctgctcgctt cagtggcagt 960
gggtctggga ccgactactc tctcacaatc aacagcttgg aggctgaaga tgctgccact 1020
tattactgcc aacagtggag tagtaacccg ctcacgttcg gtggcgggac caaggtggag 1080
atcaaaggcg aaggtactag tactggttct ggtggaagtg gaggttcagg tggagcagac 1140
gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaagggtg 1200
tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 1260
cctggacagg gtctggaatg gattggatac attaatccta gccgtgggta tactaattac 1320
gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 1380
atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 1440
gatgatcatt actgccttga ctactggggc caaggcacca cggtcacgtc ctctca 1497

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<210> 391

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> CD19xVL3VH5 HLLH

<400> 391

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Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser
1           5           10           15

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Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr
20           25           30

```

```

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35           40           45

```

Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr
130 135 140

Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile
145 150 155 160

Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu
165 170 175

Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
180 185 190

Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser
195 200 205

Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val
210 215 220

Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr
225 230 235 240

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
260 265 270

Glu Arg Ala Thr Leu Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met
275 280 285

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
290 295 300

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
305 310 315 320

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
325 330 335

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
340 345 350

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
355 360 365

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
370 375 380

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
385 390 395 400

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
405 410 415

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
420 425 430

Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe
435 440 445

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
450 455 460

Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr
465 470 475 480

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
485 490 495

Val Ser Ser

<210> 392

<211> 1497
<212> DNA
<213> artificial sequence

<220>
<223> CD19xVH7VL1 HLHL

<400> 392
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cctggacagg gtcttgagtg gattggacag atttggcctg gagatgggtga tactaactac 180
aatggaaagt tcaagggtaa agccactctg actgcagacg aatcctccag cacagcctac 240
atgcaactca gcagcctagc atctgaggac tctgcggtct atttctgtgc aagacgggag 300
actacgacgg taggocgtta ttactatgct atggactact ggggccaagg gaccacggtc 360
accgtctcct ccggtgggtg tggttctggc ggcggcggct ccggtgggtg tggttctgat 420
atccagctga ccagctctcc agcttctttg gctgtgtctc tagggcagag ggccaccatc 480
tcctgcaagg ccagccaaag tggtgattat gatggtgata gttatttgaa ctggtaccaa 540
cagattccag gacagccacc caaactcctc atctatgatg catccaatct agtttctggg 600
atcccaccca ggtttagtgg cagtgggtct gggacagact tcaccctcaa catccatcct 660
gtggagaagg tggatgctgc aacctatcac tgtcagcaaa gtactgagga tccgtggacg 720
ttcggtggag ggaccaagct cgagatcaaa tccggaggtg gtggatccga cgtccaactg 780
gtgcagtcag gggctgaagt gaaaaaacct ggggcctcag tgaagggtgc ctgcaaggct 840
tctggctaca cctttactag gtacacgatg cactgggtaa ggcaggcacc tggacagggt 900
ctggaatgga ttggatacat taatcctagc cgtgggttata ctaattacaa tcagaagttc 960
aaggaccgcg tcacaatcac tacagacaaa tccaccagca cagcctacat ggaactgagc 1020
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tgccttgact actggggcca aggcaccacg gtcaccgtct cctcaggcga aggtactagt 1140
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ccatctagcc tgtctgcac tgcggggac cgtgtcacca tcacctgcag agccagtcaa 1260
agtgtaagtt acatgaactg gtaccagcag aagccgggca aggcacccaa aagatggatt 1320
tatgacacat ccaaagtggc ttctggagtc cctgctcgct tcagtggcag tgggtctggg 1380
accgactact ctctcacaat caacagcttg gaggtgaag atgctgccac ttattactgc 1440
caacagtgga gtagtaaccc gctcacgttc ggtggcggga ccaagggtgga gatcaaa 1497

<210> 393
<211> 499
<212> PRT
<213> artificial sequence

<220>
<223> CD19xVH7VL1 HLHL

<400> 393

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr
20 25 30

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr
130 135 140

Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile
145 150 155 160

Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu
165 170 175

Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
180 185 190

Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser

195

200

205

Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val
210 215 220

Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr
225 230 235 240

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
260 265 270

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
275 280 285

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
290 295 300

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
305 310 315 320

Lys Asp Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
325 330 335

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
340 345 350

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
355 360 365

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
370 375 380

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser
385 390 395 400

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
405 410 415

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
420 425 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 435 440 445

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 450 455 460

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 465 470 475 480

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 485 490 495

Glu Ile Lys

<210> 394
 <211> 1494
 <212> DNA
 <213> artificial sequence

<220>
 <223> CD19xVL1VH7 LHLH

<400> 394
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 caacagattc caggacagcc acccaaactc ctcatctatg atgcatccaa tctagtttct 180
 gggatcccac ccaggtttag tggcagtggtg tctgggacag acttcaccct caacatccat 240
 cctgtggaga aggtggatgc tgcaacctat cactgtcagc aaagtactga ggatccgtgg 300
 acgttcggtg gagggaccaa gctcgagatc aaaggtgggtg gtggttctgg cggcggcggc 360
 tccggtgggtg gtggttctca ggtgcagctg cagcagctctg gggctgagct ggtgaggcct 420
 gggtcctcag tgaagatttc ctgcaaggct tctggctatg cattcagtag ctactggatg 480
 aactgggtga agcagaggcc tggacagggt cttgagtggg ttggacagat ttggcctgga 540
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 tcctccagca cagcctacat gcaactcagc agcctagcat ctgaggactc tgcggtctat 660
 ttctgtgcaa gacgggagac tacgacggta ggccgttatt actatgctat ggactactgg 720
 ggccaaggga ccacgggtcac cgtctcctcc ggaggtgggtg gatccgacat tcagatgacc 780
 cagtctccat ctagcctgtc tgcattctgtc ggggaccgtg tcaccatcac ctgcagagcc 840
 agtcaaagtg taagttacat gaactgggtac cagcagaagc cgggcaaggc acccaaaaga 900

tggatttatg acacatccaa agtggcttct ggagtccttg ctgccttcag tggcagtggg 960
tctgggaccg actactctct cacaatcaac agcttggagg ctgaagatgc tgccacttat 1020
tactgccaac agtggagtag taaccgcgtc acgttcggtg gcgggaccaa ggtggagatc 1080
aaaggcgaag gtactagtag tggttctggt ggaagtggag gttcaggtgg agcagacgac 1140
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tgcaaggctt ctggctacac ctttactagg tacacgatgc actgggtaag gcaggcacct 1260
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cagaagttca aggaccgcgt cacaatcact acagacaaat ccaccagcac agcctacatg 1380
gaactgagca gcctgcgttc tgaggacact gcagtctatt actgtgcaag atattatgat 1440
gatcattact gccttgacta ctggggccaa ggcaccacgg tcaccgtctc ctca 1494

<210> 395

<211> 498

<212> PRT

<213> artificial sequence

<220>

<223> CD19xVL1VH7 LHLH

<400> 395

Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
20 25 30

Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65 70 75 80

Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
85 90 95

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
115 120 125

Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val
130 135 140

Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met
145 150 155 160

Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln
165 170 175

Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly
180 185 190

Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln
195 200 205

Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg
210 215 220

Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp
225 230 235 240

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp
245 250 255

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
260 265 270

Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Tyr Met Asn
275 280 285

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp
290 295 300

Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly
305 310 315 320

Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp
325 330 335

Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe
340 345 350

Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr Gly
 355 360 365

Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu Val
 370 375 380

Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser
 385 390 395 400

Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val
 405 410 415

Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro
 420 425 430

Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr
 435 440 445

Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser
 450 455 460

Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp
 465 470 475 480

Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
 485 490 495

Ser Ser

<210> 396
 <211> 1497
 <212> DNA
 <213> artificial sequence

<220>
 <223> CD19xVL1VH7 HLLH

<400> 396
 caggtgcagc tgcagcagtc tggggctgag ctggtgaggc ctgggtcctc agtgaagatt 60
 tcttgcaagg cttctggcta tgcattcagt agctactgga tgaactgggt gaagcagagg 120
 cctggacagg gtcttgagtg gattggacag atttggcctg gagatgggtga tactaactac 180
 aatggaaagt tcaagggtaa agccactctg actgcagacg aatcctccag cacagcctac 240
 atgcaactca gcagcctagc atctgaggac tctgcggtct atttctgtgc aagacgggag 300

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actacgacgg taggccgtta ttactatgct atggactact ggggccaagg gaccacggtc   360
accgtctcct ccggtggtgg tggttctggc ggcggcggct ccggtggtgg tggttctgat   420
atccagctga ccagctctcc agcttctttg gctgtgtctc tagggcagag ggccaccatc   480
tcctgcaagg ccagccaaag tgttgattat gatggtgata gttatttgaa ctggtaccaa   540
cagattccag gacagccacc caaactcctc atctatgatg catccaatct agtttctggg   600
atcccaccca ggtttagtgg cagtgggtct gggacagact tcaccctcaa catccatcct   660
gtggagaagg tggatgctgc aacctatcac tgtcagcaaa gtactgagga tccgtggacg   720
ttcggtgagg ggaccaagct cgagatcaaa tccggaggtg gtggatccga cattcagatg   780
accagtcctc catctagcct gtctgcatct gtcggggacc gtgtcaccat cacctgcaga   840
gccagtcaaa gtgtaagtta catgaactgg taccagcaga agccgggcaa ggcacccaaa   900
agatggattt atgacacatc caaagtggct tctggagtcc ctgctcgctt cagtggcagt   960
gggtctggga ccgactactc tctcacaatc aacagcttgg aggctgaaga tgctgccact  1020
tattactgcc aacagtggag tagtaacccg ctcacgttcg gtggcgggac caaggtggag  1080
atcaaaggcg aaggtactag tactggttct ggtggaagtg gaggttcagg tggagcagac  1140
gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaagggtg  1200
tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca  1260
cctggacagg gtctggaatg gattggatac attaatccta gccgtggtta tactaattac  1320
aatcagaagt tcaaggaccg cgtcacaatc actacagaca aatccaccag cacagcctac  1380
atggaactga gcagcctgcg ttctgaggac actgcagtct attactgtgc aagatattat  1440
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctctca  1497

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<210> 397

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> CD19xVL1VH7 HLLH

<400> 397

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Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser
1           5           10          15

```

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Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr
20          25          30

```

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe
 50 55 60
 Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr
 65 70 75 80
 Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys
 85 90 95
 Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp
 100 105 110
 Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
 115 120 125
 Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr
 130 135 140
 Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile
 145 150 155 160
 Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu
 165 170 175
 Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
 180 185 190
 Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser
 195 200 205
 Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val
 210 215 220
 Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr
 225 230 235 240
 Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser
 245 250 255
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 260 265 270

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
275 280 285

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
290 295 300

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
305 310 315 320

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
325 330 335

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
340 345 350

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
355 360 365

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
370 375 380

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
385 390 395 400

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
405 410 415

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
420 425 430

Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
435 440 445

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
450 455 460

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr
465 470 475 480

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
485 490 495

Val Ser Ser

<210> 398
<211> 1497
<212> DNA
<213> artificial sequence

<220>
<223> CD19xVH7VL2 HLHL

<400> 398
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cctggacagg gtcttgagtg gattggacag atttggcctg gagatgggtga tactaactac 180
aatggaaagt tcaagggtaa agccactctg actgcagacg aatcctccag cacagcctac 240
atgcaactca gcagcctagc atctgaggac tctgcggtct atttctgtgc aagacgggag 300
actacgacgg taggccgtta ttactatgct atggactact ggggcccaagg gaccacggtc 360
accgtctect ccggtgggtg tggttctggc ggccggcggt ccggtgggtg tggttctgat 420
atccagctga ccagctctcc agcttctttg gctgtgtctc tagggcagag ggccaccatc 480
tcctgcaagg ccagccaaag tgttgattat gatggtgata gttatttgaa ctggtaccaa 540
cagattccag gacagccacc caaactcctc atctatgatg catccaatct agtttctggg 600
atcccaccca ggtttagtgg cagtgggtct gggacagact tcaccctcaa catccatcct 660
gtggagaagg tggatgctgc aacctatcac tgtcagcaaa gtactgagga tccgtggacg 720
ttcgggtggag ggaccaagct cgagatcaaa tccggaggtg gtggatccga cgtccaactg 780
gtgcagtcag gggctgaagt gaaaaaacct ggggcctcag tgaagggtgc ctgcaaggct 840
tctggctaca cctttactag gtacacgatg cactgggtaa ggcaggcacc tggacagggg 900
ctggaatgga ttggatacat taatcctagc cgtgggttata ctaattacaa tcagaagttc 960
aaggaccgcg tcacaatcac tacagacaaa tccaccagca cagcctacat ggaactgagc 1020
agcctgcgtt ctgaggacac tgcagtctat tactgtgcaa gatattatga tgatcattac 1080
tgccttgact actggggcca aggcaccacg gtcaccgtct cctcaggcga aggtactagt 1140
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ccagcaactc tgtctctgtc tccaggggag cgtgccaccc tgagctgcag agccagtcaa 1260
agtgtaagtt acatgaactg gtaccagcag aagccgggca aggcacccaa aagatggatt 1320
tatgacacat ccaaagtggc ttctggagtc cctgctcgct tcagtggcag tgggtctggg 1380
accgactact ctctcacaat caacagcttg gaggtgaag atgctgccac ttattactgc 1440

caacagtgga gtagtaaccc gctcacgttc ggtggcgggga ccaaggtgga gatcaaa 1497

<210> 399

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> CD19xVH7VL2 HLHL

<400> 399

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr
20 25 30

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr
130 135 140

Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile
145 150 155 160

Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu
165 170 175

Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr

180

185

190

Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser
 195 200 205

Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val
 210 215 220

Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr
 225 230 235 240

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser
 245 250 255

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 260 265 270

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 275 280 285

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 290 295 300

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
 305 310 315 320

Lys Asp Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
 325 330 335

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 340 345 350

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 355 360 365

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
 370 375 380

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
 385 390 395 400

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
 405 410 415

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 420 425 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 435 440 445

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 450 455 460

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 465 470 475 480

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 485 490 495

Glu Ile Lys

<210> 400
 <211> 1494
 <212> DNA
 <213> artificial sequence

<220>
 <223> CD19xVL2VH7 LHLH

<400> 400
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 caacagattc caggacagcc acccaaactc ctcatctatg atgcatccaa tctagtttct 180
 gggatcccac ccaggtttag tggcagtggtg tctgggacag acttcaccct caacatccat 240
 cctgtggaga aggtggatgc tgcaacctat cactgtcagc aaagtactga ggatccgtgg 300
 acgttcgggtg gagggaccaa gctcgagatc aaaggtgggtg gtggttcttg cggcggcggc 360
 tccggtgggtg gtggttctca ggtgcagctg cagcagttctg gggctgagct ggtgaggcct 420
 gggtcctcag tgaagatttc ctgcaaggct tctggctatg cattcagtag ctactggatg 480
 aactgggtga agcagaggcc tggacagggt cttgagtggg ttggacagat ttggcctgga 540
 gatgggtgata ctaactacaa tggaaagtgc aagggttaaag ccactctgac tgcagacgaa 600
 tcctccagca cagcctacat gcaactcagc agcctagcat ctgaggactc tgcggtctat 660
 ttctgtgcaa gacgggagac tacgacggta ggccgttatt actatgctat ggactactgg 720
 ggccaaggga ccacgggtcac cgtctcctcc ggaggtgggtg gatccgacat tgtactgacc 780

```

cagtctccag caactctgtc tctgtctcca ggggagcgtg ccaccctgag ctgcagagcc      840
agtcaaagtg taagttacat gaactgggtac cagcagaagc cgggcaaggc acccaaaaga      900
tggatttatg acacatccaa agtgggttct ggagtccttg ctgccttcag tggcagtggg      960
tctgggaccg actactctct cacaatcaac agcttggagg ctgaagatgc tgccacttat     1020
tactgccaac agtggagtag taaccgcgtc acgttcggtg gcgggaccaa ggtggagatc     1080
aaaggcgaag gtactagtag tggttctggt ggaagtggag gttcaggtgg agcagacgac     1140
gtccaactgg tgcagtcagg ggctgaagtg aaaaaacctg gggcctcagt gaaggtgtcc     1200
tgcaaggctt ctggctacac ctttactagg tacacgatgc actgggtaag gcaggcacct     1260
ggacagggtc tggaatggat tggatacatt aatcctagcc gtgggttatac taattacaat     1320
cagaagttca aggaccgctg cacaatcact acagacaaat ccaccagcac agcctacatg     1380
gaactgagca gcctgcgttc tgaggacact gcagtctatt actgtgcaag atattatgat     1440
gatcattact gccttgacta ctggggccaa ggcaccacgg tcaccgtctc ctca           1494

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<210> 401
<211> 498
<212> PRT
<213> artificial sequence

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<220>
<223> CD19xVL2VH7 LHLH

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<400> 401

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Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1           5           10           15

```

```

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
20           25           30

```

```

Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
35           40           45

```

```

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
50           55           60

```

```

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65           70           75           80

```

```

Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
85           90           95

```

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
115 120 125

Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val
130 135 140

Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met
145 150 155 160

Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln
165 170 175

Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly
180 185 190

Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln
195 200 205

Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg
210 215 220

Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp
225 230 235 240

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp
245 250 255

Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu
260 265 270

Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met Asn
275 280 285

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp
290 295 300

Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly
305 310 315 320

Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp
325 330 335

Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe
 340 345 350

Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr Gly
 355 360 365

Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu Val
 370 375 380

Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser
 385 390 395 400

Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val
 405 410 415

Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro
 420 425 430

Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr
 435 440 445

Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser
 450 455 460

Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp
 465 470 475 480

Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
 485 490 495

Ser Ser

<210> 402
 <211> 1497
 <212> DNA
 <213> artificial sequence

<220>
 <223> CD19xVL2VH7 HLLH

<400> 402
 caggtgcagc tgcagcagtc tggggctgag ctggtgaggc ctgggtcctc agtgaagatt 60
 tcctgcaagg cttctggcta tgcattcagt agctactgga tgaactgggt gaagcagagg 120
 cctggacagg gtcttgagtg gattggacag atttggcctg gagatgggtga tactaactac 180


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aatggaaagt tcaagggtaa agccactctg actgcagacg aatcctccag cacagcctac 240
atgcaactca gcagcctagc atctgaggac tctgcggtct atttctgtgc aagacgggag 300
actacgacgg taggccgtta ttactatgct atggactact ggggccaagg gaccacggtc 360
accgtctcct ccggtggtgg tggttctggc ggcggcggct ccggtggtgg tggttctgat 420
atccagctga ccagctctcc agcttctttg gctgtgtctc tagggcagag ggccaccatc 480
tcctgcaagg ccagccaaag tgttgattat gatggtgata gttatttgaa ctggtaccaa 540
cagattccag gacagccacc caaactcctc atctatgatg catccaatct agtttctggg 600
atcccaccca ggtttagtgg cagtgggtct gggacagact tcaccctcaa catccatcct 660
gtggagaagg tggatgctgc aacctatcac tgtcagcaaa gtactgagga tccgtggacg 720
ttcgggtggag ggaccaagct cgagatcaaa tccggagggtg gtggatccga cattgtactg 780
accagctctc cagcaactct gtctctgtct ccagggggagc gtgccaccct gagctgcaga 840
gccagtcaaa gtgtaagtta catgaactgg taccagcaga agccgggcaa ggcacccaaa 900
agatggattt atgacacatc caaagtggct tctggagtcc ctgctcgctt cagtggcagt 960
gggtctggga ccgactactc tctcacaatc aacagcttgg aggctgaaga tgctgccact 1020
tattactgcc aacagtggag tagtaacccg ctcacgttcg gtggcgggac caaggtggag 1080
atcaaaggcg aaggtactag tactggttct ggtggaagtg gaggttcagg tggagcagac 1140
gacgtccaac tggatgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaagggtg 1200
tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 1260
cctggacagg gtctggaatg gattggatac attaatccta gccgtgggta tactaattac 1320
aatcagaagt tcaaggaccg cgtcacaatc actacagaca aatccaccag cacagcctac 1380
atggaactga gcagcctgcg ttctgaggac actgcagtct attactgtgc aagatattat 1440
gatgatcatt actgccttga ctactggggc caaggcacca cggtcacctg ctctctca 1497

```

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<210> 403
<211> 499
<212> PRT
<213> artificial sequence

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<220>
<223> CD19xVL2VH7 HLLH

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<400> 403

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Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser
1           5           10           15

```

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr
20 25 30

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr
130 135 140

Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile
145 150 155 160

Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu
165 170 175

Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
180 185 190

Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser
195 200 205

Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val
210 215 220

Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr
225 230 235 240

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
260 265 270

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
275 280 285

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
290 295 300

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
305 310 315 320

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
325 330 335

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
340 345 350

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
355 360 365

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
370 375 380

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
385 390 395 400

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
405 410 415

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
420 425 430

Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
435 440 445

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
450 455 460

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr
465 470 475 480

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr

485

490

495

Val Ser Ser

<210> 404
<211> 1497
<212> DNA
<213> artificial sequence

<220>
<223> CD19xVH7VL3 HLHL

<400> 404
caggtgcagc tgcagcagtc tggggctgag ctggtgaggc ctgggtcctc agtgaagatt 60
tcctgcaagg cttctggcta tgcattcagt agctactgga tgaactgggt gaagcagagg 120
cctggacagg gtcttgagtg gattggacag atttggcctg gagatgggtga tactaactac 180
aatggaaagt tcaagggtaa agccactctg actgcagacg aatcctccag cacagcctac 240
atgcaactca gcagcctagc atctgaggac tctgcggtct atttctgtgc aagacgggag 300
actacgacgg taggccgtta ttactatgct atggactact ggggccaagg gaccacggtc 360
accgtctcct ccggtggtgg tggttctggc ggcggcggct ccggtggtgg tggttctgat 420
atccagctga ccagctctcc agcttctttg gctgtgtctc tagggcagag ggccaccatc 480
tcctgcaagg ccagccaaag tgttgattat gatggtgata gttatttgaa ctggtaccaa 540
cagattccag gacagccacc caaactcctc atctatgatg catccaatct agtttctggg 600
atcccaccca ggtttagtgg cagtgggtct gggacagact tcaccctcaa catccatcct 660
gtggagaagg tggatgctgc aacctatcac tgtcagcaaa gtactgagga tccgtggacg 720
ttcgggtggag ggaccaagct cgagatcaaa tccggagggtg gtggatccga cgtccaactg 780
gtgcagtcag gggctgaagt gaaaaaacct ggggcctcag tgaagggtgtc ctgcaaggct 840
tctggctaca cctttactag gtacacgatg cactgggtaa ggcaggcacc tggacagggt 900
ctggaatgga ttggatacat taatcctagc cgtgggttata ctaattacaa tcagaagttc 960
aaggaccgcg tcacaatcac tacagacaaa tccaccagca cagcctacat ggaactgagc 1020
agcctgcgtt ctgaggacac tgcagtctat tactgtgcaa gatattatga tgatcattac 1080
tgccttgact actggggcca aggcaccacg gtcaccgtct cctcaggcga aggtactagt 1140
actggttctg gtggaagtgg aggttcaggt ggagcagacg acattgtact gaccagttct 1200
ccagcaactc tgttctctgtc tccaggggag cgtgccaccc tgacctgcag agccagttca 1260
agtgtaagtt acatgaactg gtaccagcag aagccgggca aggcacccaa aagatggatt 1320

tatgacacat ccaaagtggc ttctggagtc cctgctcgct tcagtggcag tgggtctggg 1380
accgactact ctctcacaat caacagcttg gaggtgaag atgctgccac ttattactgc 1440
caacagtgga gtagtaaccc gctcacgttc ggtggcggga ccaaggtgga gatcaaa 1497

<210> 405
<211> 499
<212> PRT
<213> artificial sequence

<220>
<223> CD19xVH7VL3 HLHL

<400> 405

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr
20 25 30

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr
130 135 140

Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile
145 150 155 160

Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu

165

170

175

Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
 180 185 190

Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser
 195 200 205

Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val
 210 215 220

Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr
 225 230 235 240

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser
 245 250 255

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 260 265 270

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 275 280 285

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 290 295 300

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
 305 310 315 320

Lys Asp Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
 325 330 335

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 340 345 350

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 355 360 365

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
 370 375 380

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
 385 390 395 400

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys
405 410 415

Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
420 425 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
435 440 445

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
450 455 460

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
465 470 475 480

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
485 490 495

Glu Ile Lys

<210> 406
<211> 1494
<212> DNA
<213> artificial sequence

<220>
<223> CD19xVL3VH7 LHLH

<400> 406
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caacagattc caggacagcc acccaaactc ctcatctatg atgcatccaa tctagtttct 180
gggatccac ccaggtttag tggcagtggg tctgggacag acttcaccct caacatccat 240
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aactgggtga agcagaggcc tggacagggt cttgagtgga ttggacagat ttggcctgga 540
gatggtgata ctaactacaa tggaaagttc aagggtaaag ccactctgac tgcagacgaa 600
tcctccagca cagcctacat gcaactcagc agcctagcat ctgaggactc tgcggtctat 660

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cagaagttca aggaccgct cacaatcact acagacaaat ccaccagcac agcctacatg 1380
gaactgagca gcctgcgttc tgaggacact gcagtctatt actgtgcaag atattatgat 1440
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<210> 407

<211> 498

<212> PRT

<213> artificial sequence

<220>

<223> CD19xVL3VH7 LHLH

<400> 407

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Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1           5           10           15

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Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
20           25           30

```

```

Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
35           40           45

```

```

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
50           55           60

```

```

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65           70           75           80

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Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
85 90 95

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
115 120 125

Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val
130 135 140

Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met
145 150 155 160

Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln
165 170 175

Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly
180 185 190

Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln
195 200 205

Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg
210 215 220

Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp
225 230 235 240

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp
245 250 255

Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu
260 265 270

Arg Ala Thr Leu Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met Asn
275 280 285

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp
290 295 300

Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly
305 310 315 320

Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp
325 330 335

Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe
340 345 350

Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr Gly
355 360 365

Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu Val
370 375 380

Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser
385 390 395 400

Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val
405 410 415

Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro
420 425 430

Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr
435 440 445

Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser
450 455 460

Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp
465 470 475 480

Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
485 490 495

Ser Ser

<210> 408
<211> 1497
<212> DNA
<213> artificial sequence

<220>
<223> CD19xVL3VH7 HLLH

<400> 408
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cctggacagg gtcttgagtg gattggacag atttggcctg gagatgggtga tactaactac 180
aatggaaagt tcaagggtaa agccactctg actgcagacg aatcctccag cacagcctac 240
atgcaactca gcagcctagc atctgaggac tctgcgggtct atttctgtgc aagacgggag 300
actacgacgg taggccgtta ttactatgct atggactact ggggccaagg gaccacgggtc 360
accgtctcct ccggtgggtg tggttctggc ggccggcggt ccggtgggtg tggttctgat 420
atccagctga ccagctctcc agcttctttg gctgtgtctc tagggcagag ggccaccatc 480
tcttgcaagg ccagccaaag tggtgattat gatgggtgata gttatttgaa ctggtaccaa 540
cagattccag gacagccacc caaactcctc atctatgatg catccaatct agtttctggg 600
atcccaccca ggtttagtgg cagtgggtct gggacagact tcaccctcaa catccatcct 660
gtggagaagg tggatgctgc aacctatcac tgtcagcaaa gtactgagga tccgtggacg 720
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agatggattt atgacacatc caaagtggct tctggagtcc ctgctcgctt cagtggcagt 960
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tattactgcc aacagtggag tagtaaccgg ctcacgttcg gtggcgggac caaggtggag 1080
atcaaaggcg aaggtactag tactgggttct ggtggaagtg gaggttcagg tggagcagac 1140
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aatcagaagt tcaaggaccg cgtcacaatc actacagaca aatccaccag cacagcctac 1380
atggaactga gcagcctgcg ttctgaggac actgcagtct attactgtgc aagatattat 1440
gatgatcatt actgccttga ctactggggc caaggcacca cggtcacctg ctctctca 1497

<210> 409

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> CD19xVL3VH7 HLLH

<400> 409

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 Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr
 20 25 30
 Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe
 50 55 60
 Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr
 65 70 75 80
 Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys
 85 90 95
 Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp
 100 105 110
 Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
 115 120 125
 Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr
 130 135 140
 Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile
 145 150 155 160
 Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu
 165 170 175
 Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
 180 185 190
 Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser
 195 200 205
 Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val
 210 215 220
 Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr
 225 230 235 240

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
260 265 270

Glu Arg Ala Thr Leu Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met
275 280 285

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
290 295 300

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
305 310 315 320

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
325 330 335

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
340 345 350

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
355 360 365

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
370 375 380

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
385 390 395 400

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
405 410 415

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
420 425 430

Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
435 440 445

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
450 455 460

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr

465

470

475

480

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
485 490 495

Val Ser Ser